

Result No.	Score	Query Match	Length	DB	ID	Description
1	1320	100.0	1320	6	BD2709331	PHT receipt
2	1264.6	95.8	1335	6	BD266835	PTH funct
3	1243.2	94.2	2051	6	I17766	Sequence 3
4	1241.6	94.1	1836	10	RATPTRH	L19475 Rat parathy
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6	1158.4	87.8	2089	10	BC051981	Mus muscu
7	1155.2	87.5	2189	10	BC013446	Mus muscu
8	1153.6	87.4	1984	10	NMPHRPR	X78936 M. musculus
9	1011.2	76.6	1380	6	BD266846	PTH funct
10	983.8	74.5	1363	6	BD266847	PTH funct
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13	966.8	73.2	1948	6	CQ867504	Sequence
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DEFINITION	PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules.	linear	PAT 17-JUL-2003
ACCESSION	BD266835		
VERSION	BD266835.1	GI:33076603	
KEYWORDS	JP 2002533115-A/4.		
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 1335)		
AUTHORS	Gardella,I.J., Kronenberg,H.M., Potts,J.T. and Jueppner,H.		
TITLE	PTH functional domain conjugate peptides, derivatives thereof and novel tethered ligand-receptor molecules		
JOURNAL	Patent: JP 2002533115-A 4 08-OCT-2002;		
COMMENT	THE GENERAL HOSPITAL CORP		
	OS Artificial Sequence		
	PN JP 2002533115-A/4		
	PD 08-OCT-2002		
	PF 30-DEC-1999 JP 2000591171		
	PR 31-DEC-1998 US 60/114577		
	PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD PI JUEPPNER		
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RESULT 3
LOCUS I17766
DEFINITION Sequence 3 from patent US 5494806.
ACCESSION I17766
VERSION I17766.1 GI:1598121
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2051)
AUTHORS Segre, G.V., Kronenberg, H.M., Abou-Samra, A.-B., Juppner, H.,
Potts, J.T. Jr. and Schipani, E.
TITLE DNA and vectors encoding the parathyroid hormone receptor,
transformed cells, and recombinant production of PTHR proteins and
peptides
JOURNAL Patent: US 5494806-A 3 27-FEB-1996;
FEATURES Location/Qualifiers
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Query Match 94.2%; Score 1243.2; DB 6; Length 2051;
Best Local Similarity 99.8%; Pred. No. 3.6e-249;
Matches 1245; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 4
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LOCUS Rat parathyroid hormone/parathyroid hormone related-peptide
DEFINITION receptor mRNA, complete cds.
ACCESSION L19475
VERSION L19475.1 GI:467316
KEYWORDS parathyroid hormone; parathyroid hormone receptor; parathyroid hormone-related protein; parathyroid hormone-related receptor.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 1836)
Pausova,Z., Bourdon,J., Clayton,D., Mattei,M.G., Seldin,M.F., Janicic,N., Riviere,M., Szpirer,J., Levan,G., Szpirer,C., Goltzman,D. and Hendy,G.N.
Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (PTHr) cDNA from a rat osteosarcoma (UMR 106) cell line: chromosomal assignment of the gene in the human, mouse, and rat genomes
Genomics 20 (1), 20-26 (1994)
JOURNAL MEDLINE 94292182
PUBMED 8020952
COMMENT Original source text: Rattus norvegicus cDNA to mRNA.
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Best Local Similarity 99.7%; Pred. No. 7.8e-249; Indels 0; Gaps 0;
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ORIGIN

Query Match 87.5%; Score 1155.2; DB 10; Length 2189;

Best Local Similarity 95.4%; Pred. No. 8.4e-231;

Matches 1190; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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RESULT 8

MMHPRP

LOCUS

DEFINITION

peptide receptor.

X78936

X78936.1

GI:474828

G-protein coupled receptor; parathyroid hormone; parathyroid

hormone related peptide receptor; parathyroid hormone-related

peptide; parathyroid hormone-related protein.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Karperien, M., Van Diik, T.B., Hoeijmakers, T., Cremers, F.,

Abou-Samra, A.B., Boonstra, J., De Laat, S.W. and Defize, L.H.K.

Expression pattern of parathyroid hormone/parathyroid hormone

related peptide receptor mRNA in mouse postimplantation embryos

indicates involvement in multiple developmental processes

Unpublished

2 (bases 1 to 1984)

Karperien, M.

TITLE Direct Submission
JOURNAL Submitted (21-Apr-1994) M. Karperien, The Netherlands Inst. of Developmental, Biology, Uppsalaalaan 8, 3584 CT Utrecht, NETHERLANDS
FEATURES
Location/Qualifiers
1. 1984
/organism="Mus musculus"
/mol_type="mRNA"
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DEFINITION novel tethered ligand-receptor molecules.
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VERSION BD266846.1 GI:33076614
KEYWORDS JP 2002533115-A/15.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1380)
AUTHORS Gardella, T.J.; Kronenberg, H.M.; Potts, J.T. and Jueppner, H.
TITLE PTH functional domain conjugate peptides, derivatives thereof and
JOURNAL novel tethered ligand-receptor molecules
COMMENT Patent: JP 2002533115-A 15 08-OCT-2002;
THE GENERAL HOSPITAL CORP
OS Artificial Sequence
PN JP 2002533115-A/15
PD 08-OCT-2002
PF 30-DEC-1999 JP 2000591171

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ACCESSION			
VERSION			
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AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
Unknown.			
Unclassified.			
1 (bases 1 to 1948)			
Au-Young, J. and Sellhamer, J.J.			
Composition for the detection of signaling pathway gene expression			
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Best Local Similarity			
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86.6%; Pred. No. 1.9e-191;			
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DEFINITION
SEQUENCE 228 from Patent WO2061087.
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Sequence 228 from Patent WO2061087.
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Sequence 228 from Patent WO2061087.
AX548943

VERSION AX548943.1 GI:25813781
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Burner, G.C., Roush, C.L. and Brown, J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 228 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
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Best Local Similarity 86.6%; Pred. No. 1.9e-191;
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Search completed: July 4, 2005, 01:28:06
Job time : 5924 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2005, 15:10:00 ; Search time 788 Seconds
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Title: US-09-869-565-1

Perfect score: 1320

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
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- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004as:*
- 13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1320	100.0	1320	3	AAA58932 DNA encod
2	1260.2	95.5	1341	3	AAA51732 Tethered
3	1243.2	94.2	2051	2	AAT15947 Rat bone
4	1243.2	94.2	2051	2	AAV08390 Parathyro
5	1243.2	94.2	2051	12	ADH61258 Rat bone
6	1241.6	94.1	2065	10	ABT42039 Toxicity
7	1240	93.9	2051	2	AAQ29606 Rat bone
8	1146.4	86.8	1776	12	ADO30323 Mouse GPC
9	1006.4	76.2	1380	3	AAA51735 Human tet
10	982.2	74.4	1363	3	AAA51736 Human tet
11	979.4	74.2	1380	3	AAA51737 Human tet
12	973.4	73.7	975	3	AAA51734 Tethered
13	966.8	73.2	1948	8	ABZ42719 Human par
14	966.8	73.2	1948	10	ACA56655 Human sig
15	966.8	73.2	1948	10	ADL13887 Osteoarth
16	966.8	73.2	1948	10	ADL13875 Osteoarth
17	966.8	73.2	1948	12	ADL156451 Human pol
18	966.8	73.2	1948	13	ADR47543 Human par
19	966.8	73.2	2282	12	ADQ22747 Human sof
20	965.2	73.1	2010	2	AAV08391 Human Par

21	965.2	73.1	2010	12	ADH61259	Adh61259 Human PTH
22	965.2	73.1	2171	10	ADD71008	Add71008 Human par
23	965.2	73.1	2171	12	ADQ18188	Adq18188 Human sof
24	962	72.9	2010	2	AAT15948	Aat15948 Human kid
25	961.2	72.8	1782	10	ADL13876	Adl13876 Osteoarth
26	961.2	72.8	1782	10	ADL13886	Adl13886 Osteoarth
27	961.2	72.8	1785	12	ADQ76824	Adq76824 Human wil
28	959.6	72.7	1782	5	AB198021	Ab198021 Non-endo
29	959.6	72.7	1782	12	ADO30033	Ado30033 Human GPC
30	958.2	72.6	1779	10	ADF70391	Adf70391 Human PTH
31	946.2	71.7	2006	2	AAQ29607	Aaq29607 Human kid
32	926.6	70.1	1008	3	AAA51733	Aaa51733 Tethered
33	902.2	68.3	2177	8	ABX15515	Abx15515 cDNA enco
34	691.6	52.4	1863	2	AAT15946	Aat15946 Opossum k
35	691.6	52.4	1863	2	AAV08389	Aav08389 Parathyro
36	691.6	52.4	1863	12	ADH61257	Adh61257 Opossum k
37	690	52.3	1863	2	AAQ29605	Aaq29605 Opossum k
38	681.2	51.6	1862	2	AAT15945	Aat15945 Opossum k
39	681.2	51.6	1862	2	AAV08388	Aav08388 Parathyro
40	681.2	51.6	1862	12	ADH61256	Adh61256 Opossum k
41	678	51.4	1862	2	AAQ29604	Aaq29604 Opossum k
42	554.6	42.0	1609	3	AAA30828	Aaa30828 Zebrafish
43	554.6	42.0	1609	3	AAA49625	Aaa49625 Zebrafish
44	554.6	42.0	1609	10	ADC42304	Adc42304 cDNA enco
45	554.6	42.0	1609	10	ADH61058	Adh61058 Zebrafish

ALIGNMENTS

RESULT 1

AAA58932

ID AAA58932 standard; DNA; 1320 BP.

XX AC AAA58932;

XX AC AAA58932;

DT 20-OCT-2000 (first entry)

DE DNA encoding a mutant parathyroid hormone (PTH) receptor.

KW Mutant; parathyroid hormone; PTH; receptor; rdelantc;

KW ligand binding domain; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1308

FT sig_peptide 1..66

FT mat_peptide 67..1305

XX /*tag= a

XX /*tag= b

XX /*tag= c

XX WO200040698-A1.

XX 13-JUL-2000.

XX 31-DEC-1998; 98WO-USO27862.

XX 31-DEC-1998; 98WO-USO27862.

XX (GEHO) GEN HOSPITAL CORP.

XX Gardella TJ, Kronenberg HM, Potts JT;

XX WPI; 2000-465971/40.

XX P-PSDB; AAB07529.

XX New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a deletion of the extracellular amino-terminus ligand binding domain, useful in screening assays for identifying agonists and antagonists of PTH receptor activity.

PS Claim 2; Fig 1; 8lpp; English.

XX The present sequence encodes a mutant parathyroid hormone (PTH) receptor, designated rdelant. The polypeptide is characterised by a deletion of the extracellular amino-terminus ligand binding domain. The receptor has a minimal domain for ligand binding and is, therefore, useful in screening assays designed for the identification of agonists and antagonists of PTH receptor activity

XX SQ Sequence 1320 BP; 238 A; 402 C; 373 G; 307 T; 0 U; 0 Other;

Query Match 100.0%; Score 1320; DB 3; Length 1320;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGGCCGCGCCGAGTTCGACCCAGCCTGGCGCTCTACTCTGCTCCCGAGTCTCAGC 60

Db 1 ATGGGGCCGCGCCGAGTTCGACCCAGCCTGGCGCTCTACTCTGCTCCCGAGTCTCAGC 60

Qy 61 TCCGCATATGGCTGGAGGTATTTGACCGCTAGGCATGATCTACACCGTGGGATCTCC 120

Db 61 TCCGCATATGGCTGGAGGTATTTGACCGCTAGGCATGATCTACACCGTGGGATCTCC 120

Qy 121 ATGTCCTCGCCTCCCTCAGCTGCTGCTCATCTGCGCTATTTTAGCGGCTGCAC 180

Db 121 ATGTCCTCGCCTCCCTCAGCTGCTGCTCATCTGCGCTATTTTAGCGGCTGCAC 180

Qy 181 TGACCGGCACTACATCCACATGATTCCTGTCGTTATGTCGCGCGCGGAGC 240

Db 181 TGACCGGCACTACATCCACATGATTCCTGTCGTTATGTCGCGCGCGGAGC 240

Qy 241 ATCTTGTGAAGAGCTGTGCTTACTCTGGCTTACGCTGATGAGCGCGGCTC 300

Db 241 ATCTTGTGAAGAGCTGTGCTTACTCTGGCTTACGCTGATGAGCGCGGCTC 300

Qy 301 ACAGAGAAGATTGACATCATCGCGAGTGCACCTCGCGCGCGCTGCGCGCGTA 360

Db 301 ACAGAGAAGATTGACATCATCGCGAGTGCACCTCGCGCGCGCTGCGCGCGTA 360

Qy 361 GGCTACGCTGCTGCGCGGCTGACCTTCTCTCTACTTCTGCTGGCTTACCACTAC 420

Db 361 GGCTACGCTGCTGCGCGGCTGACCTTCTCTCTACTTCTGCTGGCTTACCACTAC 420

Qy 421 TACTGGATCTGTTGGAGGGCTGACTTGCACAGCTCATCTTCATGGCTTTTCTCA 480

Db 421 TACTGGATCTGTTGGAGGGCTGACTTGCACAGCTCATCTTCATGGCTTTTCTCA 480

Qy 481 GAGAAGAAGTACCTGTGGGGCTTACCATCTTGGCTGGGGTCTACCGGCTGCTTCGTG 540

Db 481 GAGAAGAAGTACCTGTGGGGCTTACCATCTTGGCTGGGGTCTACCGGCTGCTTCGTG 540

Qy 541 GCTGTGTGGTTCGGTGTGAGAGCACTTGGCCAACTGCGGCTGCTGGATCTGAGCTCC 600

Db 541 GCTGTGTGGTTCGGTGTGAGAGCACTTGGCCAACTGCGGCTGCTGGATCTGAGCTCC 600

Qy 601 GGGCACAAGAGTGGATCATCCAGGTGCCATCTTGGCATCTGTTGCTCACTTATC 660

Db 601 GGGCACAAGAGTGGATCATCCAGGTGCCATCTTGGCATCTGTTGCTCACTTATC 660

Qy 661 CTCTTTTATCAACATCATCCGGGCTTGGCACTAAGCTTGGGAGACCAATGCGGGCGG 720

Db 661 CTCTTTTATCAACATCATCCGGGCTTGGCACTAAGCTTGGGAGACCAATGCGGGCGG 720

Qy 721 TGTGACACCGGAGCAGTACCGAAGCTGCTCAGGTCACGTTGGTCTGTCGCGCTC 780

Db 721 TGTGACACCGGAGCAGTACCGAAGCTGCTCAGGTCACGTTGGTCTGTCGCGCTC 780

Qy 781 TTTGGTGTGACTACACCGTCTTATGCGCTTGGCTACCGAGGCTCAGGACATTG 840

Db 781 TTTGGTGTGACTACACCGTCTTATGCGCTTGGCTACCGAGGCTCAGGACATTG 840

Qy 841 TGGCAGATCCAGATGCTATGAGATGCTCTTCACTCTCTTCCAGGGATTTTTTGTGTC 900

Db 841 TGGCAGATCCAGATGCTATGAGATGCTCTTCACTCTCTTCCAGGGATTTTTTGTGTC 900

Qy 901 ATCATATCTGTTTCTGCAATGCTGAGGTGCGAGCAGAGTATAGGAAGTATGAGCGCG 960

Db 901 ATCATATCTGTTTCTGCAATGCTGAGGTGCGAGCAGAGTATAGGAAGTATGAGCGCG 960

Qy 961 TGGACACTGGCGTGTGACTTCAAGCGCAAGACGAAAGTGGAGTAGCAGCTACAGCTAT 1020

Db 961 TGGACACTGGCGTGTGACTTCAAGCGCAAGACGAAAGTGGAGTAGCAGCTACAGCTAT 1020

Qy 1021 GGCCCAATGCTGCTCACAGAGTGTCAACCAATGTGGGCCCCCGTGCAGAGCTCAGCCTC 1080

Db 1021 GGCCCAATGCTGCTCACAGAGTGTCAACCAATGTGGGCCCCCGTGCAGAGCTCAGCCTC 1080

Qy 1081 CCCTCAGCCCCCGCTGCTCTGCACTACCAATGGCCACTCCAGCTGCTGCGCAT 1140

Db 1081 CCCTCAGCCCCCGCTGCTCTGCACTACCAATGGCCACTCCAGCTGCTGCGCAT 1140

Qy 1141 GCCAAGCCAGGGCTCCAGCACTGAGACTGAAACCTACAGCTCACTATGGCGGTTCCC 1200

Db 1141 GCCAAGCCAGGGCTCCAGCACTGAGACTGAAACCTACAGCTCACTATGGCGGTTCCC 1200

Qy 1201 AAGGACGATGATTCCTTAACGGCTCTCTGCTCAGGCTGGATGAGAGGCTCCGGTCT 1260

Db 1201 AAGGACGATGATTCCTTAACGGCTCTCTGCTCAGGCTGGATGAGAGGCTCCGGTCT 1260

Qy 1261 GCGCGCGCGCTCCATGTTGAGGAGGATGGAACAGTCACTGACTGGGCACTAGG 1320

Db 1261 GCGCGCGCGCTCCATGTTGAGGAGGATGGAACAGTCACTGACTGGGCACTAGG 1320

RESULT 2

AAA51732 standard; DNA; 1341 BP.

XX AAA51732;

AC AC (first entry)

DT 31-OCT-2000 (first entry)

XX Tethered PTH-1 receptor, Tether1, coding sequence.

DE PTH; parathyroid hormone; conjugate; bone mass; bone reformation;

KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.

XX Rattus sp.

OS Synthetic.

OS Chimeric.

XX Key Location/Qualifiers

PH 1..1341

FT /*tag= a

FT /product= "Tether-1"

XX WO200039278-A2.

XX 06-JUL-2000.

XX 30-DEC-1999; 99WO-US031108.

XX 31-DEC-1998; 98US-0114577P.

XX (GARD/) GARDELLA T. J.

XX (KRON/) KRONENBERG H. M.

XX (POTT/) POTTS J. T.

XX (JUEP/) JUEPPNER H.

XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX WPI; 2000-452384/39.

XX P-PSDB; AAY96983.

XX New compound comprising an amino terminal signaling functional domain linked to a carboxy-terminal binding portion of parathyroid hormone for

PT treating mammalian conditions characterized by decreases in bone mass.
XX Claim 24; Fig 7; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)-n-B, R 1-S-(L)-n-R or S-(L)-n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether activity, increasing CAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 1341 BP; 243 A; 408 C; 380 G; 304 T; 6 U; 0 Other;

Query Match 95.58; Score 1260.2; DB 3; Length 1341;
Best Local Similarity 97.28; Pred No. 0;
Matches 1304; Conservative 1; Mismatches 3; Indels 33; Gaps 1;

QY 1 ATGGGGGCGCGCGGATCGCACCCAGCGCTGGCGCTCTCTGCTGCCAGTGCTCAGC 60
DB 1 ATGGGGGCGCGCGGATCGCACCCAGCGCTGGCGCTCTCTGCTGCCAGTGCTCAGC 60
QY 61 TCGGCATATGGCTG-----GAGGTATTGTGAC 87
DB 61 TCGGCCTATTCGGUUCGAAUCCAGUGCAUGCAUGCGGAGGAGCGAGGTATTGTGAC 120
QY 88 CGCTAGCGATGATCTACACCGTGGGATCTCCATGCTCTCGCTCCCTCACGGTGGCT 147
DB 121 CGCTAGCGATGATCTACACCGTGGGATCTCCATGCTCTCGCTCCCTCACGGTGGCT 180
QY 148 GTGCTCATCTCTGGCTATTTAGCGGCTGTCATGTCACGCGCACTACATCCACATGAC 207
DB 181 GTGCTCATCTCTGGCTATTTAGCGGCTGTCATGTCACGCGCACTACATCCACATGAC 240
QY 208 ATGTTCTCTGCTGTTATGCTGCGGCGCGGAGGATCTTCGTAAGGAGCGTGTCTTAC 267
DB 241 ATGTTCTCTGCTGTTATGCTGCGGCGCGGAGGATCTTCGTAAGGAGCGTGTCTTAC 300
QY 268 TCTGGCTTCACGCTGAGTGGCGGAGCGCTCTACAGAGGAAGTTCACATCATCGCG 327
DB 301 TCTGGCTTCACGCTGAGTGGCGGAGCGCTCTACAGAGGAAGTTCACATCATCGCG 360
QY 328 CAGGTGCCACCTCCCGCGCGCGCTGCGCGGCTAGGCTACGCTGCGCGGCTGGCGGCTG 387
DB 361 CAGGTGCCACCTCCCGCGCGCGCTGCGCGGCTAGGCTACGCTGCGCGGCTGGCGGCTG 420
QY 388 ACCTTCTCTCTACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 447
DB 421 ACCTTCTCTCTACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 448 TTGCACAGCTCATCTTCTCATGGCTTTTCTCAGAGGAAGTACCTGCGGGCTTCACC 507
DB 481 TTGCACAGCTCATCTTCTCATGGCTTTTCTCAGAGGAAGTACCTGCGGGCTTCACC 540
QY 508 ATCTTTTGGCTGGGCTTACCGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 567
DB 541 ATCTTTTGGCTGGGCTTACCGGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 568 TTGGCCAACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 627
DB 601 TTGGCCAACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 628 CCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 687
DB 661 CCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

QY 688 GCACCTAAGCTTCGGGAGAGCAATGCGGCGCGGTGTGACACACAGGACGAGTACCGGAAG 747
DB 721 GCACCTAAGCTTCGGGAGAGCAATGCGGCGCGGTGTGACACACAGGACGAGTACCGGAAG 780
QY 748 CTGCTCAGGTCCACGCTTGGTGTCTGCGCGCTCTTTGGTGTGACACTACCGTCTTCATG 807
DB 781 CTGCTCAGGTCCACGCTTGGTGTCTGCGCGCTCTTTGGTGTGACACTACCGTCTTCATG 840
QY 808 GCCTTGCCTGTACACCGAGGTCTCAGGAGACATTTGGGAGATCCAGATGCAATTAGAGATG 867
DB 841 GCCTTGCCTGTACACCGAGGTCTCAGGAGACATTTGGGAGATCCAGATGCAATTAGAGATG 900
QY 868 CTCTTCACTCTCTCCAGGAGATTTTGTGGCATCATATCTGTTCTGCAATGGTGAG 927
DB 901 CTCTTCACTCTCTCCAGGAGATTTTGTGGCATCATATCTGTTCTGCAATGGTGAG 960
QY 928 GTGCGGACAGAGATTAGGAGTCTATGAGCGCGCTGGACACTGGCGTTGGAGCTTCAAGCGC 987
DB 961 GTGCGGACAGAGATTAGGAGTCTATGAGCGCGCTGGACACTGGCGTTGGAGCTTCAAGCGC 1020
QY 988 AAAGCAGAGAGTGGGAGTAGCAGCTACAGCTATGCGCCCAATGGTGTCTCACAGAGTGTG 1047
DB 1021 AAAGCAGAGAGTGGGAGTAGCAGCTACAGCTATGCGCCCAATGGTGTCTCACAGAGTGTG 1080
QY 1048 ACCAATGTGGGCGCGCGTGGAGACTCAGCTCTCCCTCAGCCCCCGCTGCTCTCTGCC 1107
DB 1081 ACCAATGTGGGCGCGCGTGGAGACTCAGCTCTCCCTCAGCCCCCGCTGCTCTCTGCC 1140
QY 1108 ACTACCAATGGCGCACCTCCAGCTGCGCATGCCAAGCCAGGGGCTCCAGGCCACTGAG 1167
DB 1141 ACTACCAATGGCGCACCTCCAGCTGCGCATGCCAAGCCAGGGGCTCCAGGCCACTGAG 1200
QY 1168 ACTGAAACCCCTACAGTCACTATGCGGCTTCCCAAGGACGATGGATTCCTTAACGGCTCC 1227
DB 1201 ACTGAAACCCCTACAGTCACTATGCGGCTTCCCAAGGACGATGGATTCCTTAACGGCTCC 1260
QY 1228 TGCTCAGGCTGTGATGAGGAGGCTTCCGGGTCTGCGGCGCGCTCCATTGTTGCAGAA 1287
DB 1261 TGCTCAGGCTGTGATGAGGAGGCTTCCGGGTCTGCGGCGCGCTCCATTGTTGCAGAA 1320
QY 1288 GGATGGGAACAGTCAATGTA 1308
DB 1321 GGATGGGAACAGTCAATGTA 1341
RESULT 3
AAT15947
ID AAT15947 standard; cDNA; 2051 BP.
XX
AC AAT15947;
AC AC
XX XX
DT 25-MAR-2003 (revised)
DT 18-MAY-1996 (first entry)
XX XX
DE Rat bone PTH/PTHrP receptor cDNA clone R15B.
XX XX
KW Parathyroid hormone; receptor; parathormone; PTH;
KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
KW hypercalcaemia; hypocalcaemia; cancer; transgenic animal;
XX transgenic fowl; db.
XX Rattus sp.
XX OS
XX XX
PH Key Location/Qualifiers
FT CDS 73..1848
FT /*tag= a
XX
XX US5494806-A.
XX
XX 27-FEB-1996.
XX
XX 06-APR-1992; 92US-00864475.
XX
XX

PR 05-APR-1991; 91US-00681702.
XX (GEHO) GEN HOSPITAL CORP.
PA Potts JT, Juppner H, Segre GV, Schipani E, Kronenberg HM;
PI Abou-Samra A;
XX MPI; 1996-1139028/14.
DR P-PSDB; AAR92277.
XX
XX DNA encoding vertebrate parathyroid hormone receptor - useful for
XX diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia, cancer
XX etc.
XX Claim 1; Fig 3A-3E; 64pp; English.
XX
XX A cDNA clone (AAT15947), designated R15B ATCC 68571, codes for a rat
XX parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
XX receptor (AAR92277). To obtain R15B, a rat osteosarcoma ROS 17/2.8 cDNA
XX library in pcDNA1 was used to transfect COS cells, and transfectants were
XX selected for ability to bind labelled PTH. Recombinant receptor is
XX produced in vector/host cell systems. The host cells can be used for
XX diagnostic measurement of PTH serum levels. Transgenic chickens that
XX overexpress the receptor in their oviduct lay eggs of higher calcium
XX content. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 2051 BP; 429 A; 575 C; 616 G; 431 T; 0 U; 0 Other;
XX
XX Query Match 94.2%; Score 1243.2; DB 2; Length 2051;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 1245; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 73 CTGGAGGTATTGACCCCTAGGATGATCTACACCGTGGGATCTCCATGCTCTCGCC 132
XX |
XX 613 CGGAGGTATTGACCCCTAGGATGATCTACACCGTGGGATCTCCATGCTCTCGCC 672
XX |
XX 133 TCCCTCAGCGTGGCTGCTCATCTCGCTCTATTTAGGCGGCTGCACTCAGCGCAAC 192
XX |
XX 673 TCCCTCAGCGTGGCTGCTCATCTCGCTCTATTTAGGCGGCTGCACTCAGCGCAAC 732
XX |
XX 193 TACATCCACATGACATGTTCTCTGTTTATGCTGCGCCGCGAGCATCTTCTGTAAG 252
XX |
XX 733 TACATCCACATGACATGTTCTCTGTTTATGCTGCGCCGCGAGCATCTTCTGTAAG 792
XX |
XX 253 GACGCTGTCTACTCTGCTTTCAGCTGATGAGCGCGCTTACAGAGGAGAG 312
XX |
XX 793 GACGCTGTCTACTCTGCTTTCAGCTGATGAGCGCGCTTACAGAGGAGAG 852
XX |
XX 313 TTGCACATCATCGCGCAGGTGCCACCTCCGCGCGCGCTGCGCGCTAGGCTAGCTGGC 372
XX |
XX 853 TTGCACATCATCGCGCAGGTGCCACCTCCGCGCGCGCTGCGCGCTAGGCTAGCTGGC 912
XX |
XX 373 TGCCGCGTGGCGGTGACCTTCTTCTCTACTTCTGCTACCAACTACTACTGATCCTG 432
XX |
XX 913 TGCCGCGTGGCGGTGACCTTCTTCTCTACTTCTGCTACCAACTACTACTGATCCTG 972
XX |
XX 433 GTGAGGGGCTGTACTTGCACAGCTCATCTTCAATGSCCTTTTCTCAGAGAGAGTAC 492
XX |
XX 973 GTGAGGGGCTGTACTTGCACAGCTCATCTTCAATGSCCTTTTCTCAGAGAGAGTAC 1032
XX |
XX 493 CTGTGGGGCTTACCATCTTTGGCTGGGTCTACCGGCTGTCTTGGGTGTGTGGGTGTC 552
XX |
XX 1033 CTGTGGGGCTTACCATCTTTGGCTGGGTCTACCGGCTGTCTTGGGTGTGTGGGTGTC 1092
XX |
XX 553 GGTGTACAGACCACTTTGGCCAACTGGGTGTGGGTCTGAGCTCCGGGCAAGAG 612
XX |
XX 1093 GGTGTACAGACCACTTTGGCCAACTGGGTGTGGGTCTGAGCTCCGGGCAAGAG 1152
XX |
XX 613 TGGATCATTCAGGTGCGGCTCTGGGATCTGTTGTGCTCACTTCTTATCAAC 672
XX |
XX 1153 TGGATCATTCAGGTGCGGCTCTGGGATCTGTTGTGCTCACTTCTTATCAAC 1212
XX |
XX 673 ATATCCGGGTGCTTGCCACTTAAGCTTTCGGGAGACCAATGCGGCGGTGTGACACCAAG 732

RESULT 4

AAV08390

ID AAV08390 standard; DNA; 2051 BP.

XX AC AAV08390;

XX AC AC (first entry)

XX 08-FEB-1999 (first entry)

XX Parathyroid hormone receptor R15B coding sequence.

XX Parathyroid hormone receptor; PTH receptor; antibody; therapy;

XX PTH-related hypercalcaemia; rat; ds.

XX Rattus sp.

XX Key Location/Qualifiers

XX CDS 73..1848

XX /*tag= a

XX US5840853-A.

XX 24-NOV-1998.

XX 06-JUN-1995; 95US-00471494.

XX 05-APR-1991; 91US-00681702.

XX 06-APR-1992; 92US-00864475.

XX (GEHO) GEN HOSPITAL CORP.

XX PA

XX Abou-Samra A, Juppner H, Potts JT, Segre GV, Schipani E;
PI Kronenberg HM;
XX WPI; 1999-034124/03.
DR P-PSDB; AAW73316.
DR Antikbody to parathyroid hormone receptor - for diagnostic or therapeutic
XX use.
PT Claim 6; Fig 3; 63pp; English.
XX This sequence encodes the rat parathyroid hormone (PTH) receptor R15B,
PS which is targeted by the antibody of the invention. The antibody of the
XX invention is immunoreactive with naturally occurring human, rat or
CC opossum PTH receptor. The antibody is useful for treating disorders
CC characterised by overstimulation of PTH receptors by their ligand and for
CC the diagnosis of PTH-related hypercalcaemia
XX
SQ Sequence 2051 BP; 429 A; 575 C; 616 G; 431 T; 0 U; 0 Other;
Query Match 94.2%; Score 1243.2; DB 2; Length 2051;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1245; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
73 CTGAGGTATTGACCGCTAGGCGATGATCTACACCGTGGGATCTCCATGTCTCTCGCC 132
613 CGGAGGTATTGACCGCTAGGCGATGATCTACACCGTGGGATCTCCATGTCTCTCGCC 672
133 TCCCTCAGGTGGTGTCT 192
673 TCCCTCAGGTGGTGTCT 732
193 TACATCCACATGACATGTTCT 252
733 TACATCCACATGACATGTTCT 792
253 GACGCTGTCTTACTCTGGCTTACGCTGATGAGCGCGCGCTTACAGAGGAAGAG 312
793 GACGCTGTCTTACTCTGGCTTACGCTGATGAGCGCGCGCTTACAGAGGAAGAG 852
313 TTGCACATCATCGCGAGGTGCGACCTCCGCGCGCGCGCTGCGCGGTAGGCTAGCTGGC 372
853 TTGCACATCATCGCGAGGTGCGACCTCCGCGCGCGCGCTGCGCGGTAGGCTAGCTGGC 912
373 TGCGCGTGGCGGTGACTTCT 432
913 TGCGCGTGGCGGTGACTTCT 972
433 GTGAGGGGCTGTACTTGCACAGCTCTCATCTTCAATGGCCCTTTTCTCAGAGGAAGTAC 492
973 GTGAGGGGCTGTACTTGCACAGCTCTCATCTTCAATGGCCCTTTTCTCAGAGGAAGTAC 1032
493 CTGTGGGGCTTACCATCTTTGGCTGGGGTCTACCGGCTGTCTTCTGTGGCTGTGGGTC 552
1033 CTGTGGGGCTTACCATCTTTGGCTGGGGTCTACCGGCTGTCTTCTGTGGCTGTGGGTC 1092
553 GGTGTGAGCAACCTTGGCCCACTGGGTGCTGGGATCTGAGCTCGGGGCAAGAG 612
1093 GGTGTGAGCAACCTTGGCCCACTGGGTGCTGGGATCTGAGCTCGGGGCAAGAG 1152
613 TGGATCATTCAGGTGCGCATCTGGCATCTGTGTGTCTCAACTTCATCTCTTTTATCAAC 672
1153 TGGATCATTCAGGTGCGCATCTGGCATCTGTGTGTCTCAACTTCATCTCTTTTATCAAC 1212
673 ATCATCCGGGTGCTTGGCACTTAAGCTTGGGAGACCAATGCGGGCGGGTGTGACACAGG 732
1213 ATCATCCGGGTGCTTGGCACTTAAGCTTGGGAGACCAATGCGGGCGGGTGTGACACAGG 1272
733 CAGCAGTACCGGAGCTGCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGT 792
1273 CAGCAGTACCGGAGCTGCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGTCTCAGT 1332

QY 793 TACACCGCTTTCATGGCCTTGCCTACACCGAGGTCTCAGGAGCATTTGTGGCAGATCCAG 852
DB 1333 TACACCGCTTTCATGGCCTTGCCTACACCGAGGTCTCAGGAGCATTTGTGGCAGATCCAG 1392
QY 853 ATGCAATTATGAGATGCTCTTCAACTCTCTCCAGGATTTTTTTTGTGGCATCATATACTGT 912
DB 1393 ATGCAATTATGAGATGCTCTTCAACTCTCTCCAGGATTTTTTTTGTGGCATCATATACTGT 1452
QY 913 TTCTGCAATGGTGAAGTGCAGGAGATTAGGAAGTTCATGGAGCCGCTCGACACTGGCG 972
DB 1453 TTCTGCAATGGTGAAGTGCAGGAGATTAGGAAGTTCATGGAGCCGCTCGACACTGGCG 1512
QY 973 TTGGACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCTATGCCCCCAATGGTG 1032
DB 1513 TTGGACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCTATGCCCCCAATGGTG 1572
QY 1033 TCTCACACGAGTGTGACCAATGTGGGCCCGCTGAGGACTCAGCCCTCCCTCAGGCC 1092
DB 1573 TCTCACACGAGTGTGACCAATGTGGGCCCGCTGAGGACTCAGCCCTCCCTCAGGCC 1632
QY 1093 CGCTGCTCTCTGCCACTACCAATGGCCACTCCCGAGCTGCTGGCCATGCCAAGCCAGGG 1152
DB 1633 CGCTGCTCTCTGCCACTACCAATGGCCACTCCCGAGCTGCTGGCCATGCCAAGCCAGGG 1692
QY 1153 GCTCCAGCCACTGAGACTGAAACCCCTACAGTCACTATGCGCGTTCCTCAAGGACGATGGA 1212
DB 1693 GCTCCAGCCACTGAGACTGAAACCCCTACAGTCACTATGCGCGTTCCTCAAGGACGATGGA 1752
QY 1213 TTCTTAAACGGCTCTGCTCAGGCCCTGAGGAGGAGCCCTCCCGGTCTGCGCGCCGCT 1272
DB 1753 TTCTTAAACGGCTCTGCTCAGGCCCTGAGGAGGAGCCCTCCCGGTCTGCGCGCCGCT 1812
QY 1273 CCATTGTTGAGGAGGATGGGAAACAGTCACTGCTGGGCACTAGG 1320
DB 1813 CCATTGTTGAGGAGGATGGGAAACAGTCACTGCTGGGCACTAGG 1860
RESULT 5
ADH61258
ID ADH61258 standard; cDNA; 2051 BP.
XX
AC ADH61258;
XX
DT 25-MAR-2004 (first entry)
XX
DE Rat bone PTH/PTHrP receptor cDNA clone, R15B.
XX
KW osteopathic; Parathyroid hormone receptor; hypercalcaemia;
KW hyperparathyroidism; osteoporosis; carcinoma; epidermoid cancer;
KW oesophagus multiple myeloma; hypocalcaemia; gene; cytostatic; rat; PTH;
KW PTHrP; PTH-related protein; ss.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT CDS 73..1848
FT /tag= a
FT /product= "Rat bone PTH/PTHrP receptor protein"
XX
PN US2003153041-A1.
XX
PD 14-AUG-2003.
XX
PF 09-OCT-2002; 2002US-00267730.
XX
PR 05-APR-1991; 91US-00681702.
PR 06-APR-1992; 92US-00864475.
PR 06-JUN-1995; 95US-00471494.
PR 24-NOV-1998; 98US-00199874.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Segre GV, Kronenberg HM, Abou-Samra A, Juppner H, Potts JT;

KW Parathyroid hormone; related protein; calcium; antagonist; antibodies;
KW hypercalcaemia; ss.
XX
XX Rattus rattus.
XX
XX Key Location/Qualifiers
XX CDS 73..1848
XX /*tag= a
XX
XX W09217602-A1.
XX
XX 15-OCT-1992.
XX
XX 06-APR-1992; 92WO-US002821.
XX
XX 05-APR-1991; 91US-00681702.
XX
XX (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
XX
XX Segre GV, Kronenberg HM, Abou-Samra A, Juppner H, Potts JT;
XX Schipani E;
XX
XX WPI; 1992-366271/44.
XX
XX P-PSDB; AAR27706.
XX
XX New DNA encoding parathyroid hormone receptor, DNA and antibodies - for
XX (differential) diagnosis of hypercalcaemia, and diagnosis and treatment
XX of tumours.
XX
XX Claim 3; Fig 3; 9lpp; English.
XX
XX Total RNA was isolated from rat osteosarcoma (ROS) cells and used to
XX prep. a cDNA library. The resultant phage libraries were used to
XX transform E. coli contg. a larger helper plasmid p3. The cells were
XX screened to isolate those expressing functionally intact ROS cell
XX parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
XX receptor proteins, performed according to Gearing et al., (EMBO J. 8:
XX 3676, 1989), by identifying colonies capable of binding a suitable
XX therapeutically ligand. The clone encodes a protein which may be used in a
XX therapeutic compen. to inhibit activation of PTH or PTHrP and thus reduce
XX the level of calcium in the blood. Cops. capable of competing with PTH or
XX PTHrP for binding can be identified using the protein prod. and DNAs
XX homologous to PTH DNA can be identified using fragments of the clone as
XX probes. The sequence may be used for the prodn. of antibodies useful for
XX the treatment, classification, prognosis and/or treatment of disorders
XX related to the interaction between a cell receptor and a ligand such as
XX in hypercalcaemia. See also AAO29604-11. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX
XX SQ Sequence 2051 BP; 430 A; 576 C; 616 G; 429 T; 0 U; 0 Other;
Query Match 93.9%; Score 1240; DB 2; Length 2051;
Best Local Similarity 99.6%; Pred. No. 5.7e-314;
Matches 1243; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 73 CTGAGGATTTTACCGCGTAGGCGATGATACACCGTGGGATCTCATGCTCTCGCC 132
DB 613 CGGGAGGATTTTACCGCGTAGGCGATGATACACCGTGGGATCTCATGCTCTCGCC 672
QY 133 TCCCTCAGCGTGGCTGTGCTCATCTCGCTTATTTAGGCGGCTGACGTCACGCGCAAC 192
DB 673 TCCCTCAGCGTGGCTGTGCTCATCTCGCTTATTTAGGCGGCTGACGTCACGCGCAAC 732
QY 193 TACATCCACATGACATGTTCTCTGCTTTATGCTGCGCGCGCGAGCATCTTCGTGAAG 252
DB 733 TACATCCACATGACATGTTCTCTGCTTTATGCTGCGCGCGCGAGCATCTTCGTGAAG 792
QY 253 GACGCTGTCTACTCTGGCTTCACGCTGATGAGCGCGGCGCTTCACAGGAAGAG 312
DB 793 GACGCTGTCTACTCTGGCTTCACGCTGATGAGCGCGGCGCTTCACAGGAAGAG 852
QY 313 TTGCACATCATCGCGCAGGTGCCACCTCCGCGCGCGCTGCGCGCTAGGCTAGCTGGC 372

DB 853 TTGCACATCATCGCGCAGGTGCGCACTCGCGCGCGCTGCGCGCTAGCTACGCTGGC 912
QY 373 TGCCGCTGGCGGTGACCTTCTCTACTTCTCTGCTACCACTACTACTACTGATCTCTG 432
DB 913 TGCCGCTGGCGGTGACCTTCTCTACTTCTCTGCTACCACTACTACTACTGATCTCTG 972
QY 433 GTGGAGGGGCTGTACTTTCACAGCGCTTCTCATGCGCTTTTCTCAGAGAAGAAGTAC 492
DB 973 GTGGAGGGGCTGTACTTTCACAGCGCTTCTCATGCGCTTTTCTCAGAGAAGAAGTAC 1032
QY 493 CTGTGGGGCTTTCACCATCTTTGGCTGGGGTCTACCGGCTGTCTTCGTGGCTGTGGGTC 552
DB 1033 CTGTGGGGCTTTCACCATCTTTGGCTGGGGTCTACCGGCTGTCTTCGTGGCTGTGGGTC 1092
QY 553 GGTGTGAGAGCAACCTTTGGCCAAACACTGGGTGCTGGGATCTGAGCTCCGGGCAAGAAG 612
DB 1093 GGTGTGAGAGCAACCTTTGGCCAAACACTGGGTGCTGGGATCTGAGCTCCGGGCAAGAAG 1152
QY 613 TGGATCATCCAGGTGCCCATCTCTGGCATCTGTTGTGCTCAACTTCACTCTTTTATCAAC 672
DB 1153 TGGATCATCCAGGTGCCCATCTCTGGCATCTGTTGTGCTCAACTTCACTCTTTTATCAAC 1212
QY 673 ATCATCCGGTGTCTTGCCACTTAAGCTTCGGGAGACCAATCGCGCGCGGTGTGACACAGG 732
DB 1213 ATCATCCGGTGTCTTGCCACTTAAGCTTCGGGAGACCAATCGCGCGCGGTGTGACACAGG 1272
QY 733 CAGCAGTACCGGAAGCTGTCTCAGGTCCAGTTCAGTGGTGTCTGTCGCGCTCTTTGGTGTGCAC 792
DB 1273 CAGCAGTACCGGAAGCTGTCTCAGGTCCAGTTCAGTGGTGTCTGTCGCGCTCTTTGGTGTGCAC 1332
QY 793 TACACGCTCTTCATGGCTTTCGCGTACACGAGGTCTCAGGGGACATTTGTGGCAGATCCAG 852
DB 1333 TACACGCTCTTCATGGCTTTCGCGTACACGAGGTCTCAGGGGACATTTGTGGCAGATCCAG 1392
QY 853 ATGCATTATGAGATGTCTTCAACTCTCTCCAGGGATTTTGTGTGCCATCATATACTGT 912
DB 1393 ATGCATTATGAGATGTCTTCAACTCTCCAGCGAGGATTTTGTGTGCCATCATATACTGT 1452
QY 913 TTCTGCAATGGTGTGAGGTGACGAGAGATTAGGAAGTCTAGGAGCGCTGGGACACTGGCG 972
DB 1453 TTCTGCAATGGTGTGAGGTGACGAGAGATTAGGAAGTCTAGGAGCGCTGGGACACTGGCG 1512
QY 973 TTGCACTTCAAGCGCAAGACGCAAGTGGGAGTAGCAGCTACAGCTATGGCCCAATGGTG 1032
DB 1513 TTGCACTTCAAGCGCAAGACGCAAGTGGGAGTAGCAGCTACAGCTATGGCCCAATGGTG 1572
QY 1033 TCTCACACGAGTGTGACCAATGTGGGCCCGCGTGCAGGACTCAGCTTCCCTTCAGCCCC 1092
DB 1573 TCTCACACGAGTGTGACCAATGTGGGCCCGCGTGCAGGACTCAGCTTCCCTTCAGCCCC 1632
QY 1093 CGCTGCTCTCTGCGCACTACCAATGGCCACTCCAGCTGCGCTGGCCATGCCAAGCCAGGG 1152
DB 1633 CGCTGCTCTCTGCGCACTACCAATGGCCACTCCAGCTGCGCTGGCCATGCCAAGCCAGGG 1692
QY 1153 GCTCCAGCCACTCAGACTGAAACCCCTACAGTCACTATATGGCGGTTCCTCAAGGACGATGGA 1212
DB 1693 GCTCCAGCCACTCAGACTGAAACCCCTACAGTCACTATATGGCGGTTCCTCAAGGACGATGGA 1752
QY 1213 TTCTTTAAACGGCTCTCTGCTCAGGCTTGGATGAGGAGCGCTCCCGGCTGTGCGCGCGCCT 1272
DB 1753 TTCTTTAAACGGCTCTCTGCTCAGGCTTGGATGAGGAGCGCTCCCGGCTGTGCGCGCGCCT 1812
QY 1273 CCATTGTTGAGGAAGATGGGAAACAGTCACTGTGACTGGGCACTAGG 1320
DB 1813 CCATTGTTGAGGAAGATGGGAAACAGTCACTGTGACTGGGCACTAGG 1860
RESULT 8
ADO30323
ID ADO30323 standard; cDNA; 1776 BP.
XX
XX ADO30323;
XX

DT	29-JUL-2004	(first entry)	
XX	Mouse GPCR PTHR1 polynucleotide, SEQ ID NO:1426.		
DE			
XX			
XX			
KW	G protein-coupled receptor; GPCR; drug screening; diagnosis;		
KW	transgenic mouse; neurological disorder; adrenal gland disorder;		
KW	colon disorder; intestinal disorder; cardiovascular disorder;		
KW	muscular disorder; blood disorder; immune disorder; bone disorder;		
KW	joint disorder; metabolic disorder; nutritive disorder; cancer;		
KW	kidney disorder; liver disorder; lung disorder; breast disorder;		
KW	ovary disorder; uterus disorder; prostate disorder; testis disorder;		
KW	skin disorder; stomach disorder; pancreas disorder; spleen disorder;		
KW	thymus disorder; thyroid disorder; antiparkinsonian; antineoplastic;		
KW	cystostatic; antinflammatory; vasotropic; antianginal; antiarrhythmic;		
KW	CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;		
KW	virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;		
KW	dermatological; antitumor; antithyroid; antiallergic; anorectic;		
KW	immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;		
KW	murine; gene; ss.		
XX			
OS	Mus musculus.		
XX			
XX	WO2004040000-A2.		
PN			
XX			
PD	13-MAY-2004.		
XX			
PF	09-SEP-2003; 2003WO-US028226.		
XX			
XX	09-SEP-2002; 2002US-0409303P.		
PR	09-APR-2003; 2003US-0461329P.		
XX			
PA	(PRIM-) PRIMAL INC.		
XX			
PI	Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li P;		
PI	Madisen L, McIlwain KL, Pavlova MN, Vaessilatis D, Zeng H;		
XX			
DR	WPI; 2004-390329/36.		
DR	P-PSDB; ADO29629.		
XX			
PT	Novel mammalian G protein coupled receptors, useful for identifying		
PT	compounds that modulates diagnosing and treating disease condition		
PT	associated with GPCR dysfunction e.g. autoimmune diseases, angina		
PT	pectoris, Parkinson's disease.		
XX			
PS	Claim 151; SEQ ID NO 1426; 542pp; English.		
XX			
CC	The invention relates to human and mouse G protein-coupled receptors		
CC	(GPCRs) and nucleic acids encoding them. The invention also relates to		
CC	sequences at least 90% identical to the GPCR proteins and nucleic acids		
CC	of the invention; methods of treating, preventing or diagnosing diseases		
CC	associated with GPCRs of the invention; methods of screening for		
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic		
CC	mouse comprising a GPCR gene of the invention, a mouse comprising a		
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived		
CC	from the transgenic mice; kits comprising several mice, each of which has		
CC	a mutation in a different GPCR gene of the invention; and kits comprising		
CC	probes which hybridise to GPCR polynucleotides of the invention. The		
CC	invention further discloses variants of the GPCR polypeptides and vectors		
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may		
CC	be used in the diagnosis, treatment or prevention of a wide variety of		
CC	diseases including neurological disorders (e.g., Alzheimer's disease,		
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);		
CC	disorders of the adrenal gland; disorders of the colon or intestine		
CC	(e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel		
CC	syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or		
CC	myocardial infarction); muscual disorders; blood disorders (e.g.,		
CC	anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or		
CC	AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid		
CC	arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,		
CC	obesity, enzyme deficiency-related diseases or vitamin deficiency-related		
CC	diseases); and disorders of the kidney, liver, lung, breast, ovary,		
CC	uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and		
CC	thyroid (e.g., cancers). The present sequence represents a GPCR-encoding		

Db 1441 TTGGACTTCAAGCTAAAGACGAAAGTGGAGTAGCAGCTACAGCTATGTGCCCAATGGGT 1500
Qy 1033 TCTCACAGAGTGTGACCAATGTGGGCCCGCGTGCAGGACTCAGCTCCCTCAGCCCC 1092
Db 1501 GCACACAGAGTGTGACCAATGTGGGCCCGCGTGCAGGACTCAGCTTCCCTTAGCCCC 1560
Qy 1093 CGCTGCTCTCTGCGCACTTACCAATGGCCACTCCAGAGTGTGGCCATGCAAGCCAGGG 1152
Db 1561 CGCTGCTCTCTGCGCACTTACCAATGGCCACTCCAGAGTGTGGCCATGCAAGCCAGGG 1620
Qy 1153 GCTCCAGCCACTGAGACTGAAACCTTACCAGTCACTATGCGGTTCCTCAAGGACGATGGA 1212
Db 1621 GCTCCAGCCACTGAGAAACCAATACCACTTACTATGACAGTTCCCAAGGACGAGCGC 1680
Qy 1213 TTCTTAACGGCTCTCTCAGGCTGATGAGAGCCCTCCGGTCTGCGCGCCGCT 1272
Db 1681 TTCTTAATGGCTCTCTCAGGCTGATGAGAGCCCTCTGGTCTGCGCGCCACCT 1740
Qy 1273 CCATTGTTGAGGAAGGATGGAAACAGTCATGGA 1308
Db 1741 CCATTGTTGAGGAAGGATGGAAACAGTCATGGA 1776

RESULT 9

AAA51736
ID AAA51736 standard; DNA; 1380 BP.
XX AC
AC AAA51736;

31-OCT-2000 (first entry)

Human tethered PTH-1 receptor, hdelNT, coding sequence.

XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.
XX OS

XX Homo sapiens.
XX Synthetic.
XX Chimeric.

Key Location/Qualifiers
CDS 28..1335
FT /*tag= a
FT /product= "hdelNT"

XX WO200039278-A2.

XX 06-JUL-2000.

XX 30-DEC-1999; 99WO-US031108.

XX 31-DEC-1998; 98US-0114577P.

XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.

XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX WPI; 2000-452384/39.
XX P-PSDB; AAY96987.

XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass.

XX Example 4; Fig 18; 119pp; English.

XX Compounds of the structure or formula S-(L)_n-B, R 1-S-(L)_n-R or S-(L)_n-
XX -R, are new. S is an amino terminal signaling functional domain of
XX parathyroid hormone (PTH); L is a linker molecule present n times (where
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding

CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrp which avoids the need for
CC regular injections to treat osteoporosis

XX SQ Sequence 1380 BP; 245 A; 464 C; 388 G; 283 T; 0 U; 0 Other;

Query Match 76.2%; Score 1006.4; DB 3; Length 1380;
Best Local Similarity 86.6%; Pred. No. 6.3e-253;
Matches 1148; Conservative 0; Mismatches 166; Indels 12; Gaps 3;

Qy 1 ATGGGGGCGCGCGGATCGCACCGCTGGGCTCCTACTCTGTGCCAGTGTCTCAGC 60
Db 28 ATGGGGACCGCGCGGATCGCACCGGCTGGGCTCCTGTCTGTGCGCGCTCAGC 87
Qy 61 TCCGCATATGCGCTGAGGATTTGACCGCTAGGATGATCTACACCGTGGGATCTCC 120
Db 88 TCCGCATAT-----GAGGTGTTGACCGCTGGGCTGATTTACACCGTGGGCTACTCC 141
Qy 121 ATGTCTCTCGCTCCCTCAGCGTGGCTGTGCTCATCTGGCCCTATTTTAGCGGCTGCAC 180
Db 142 GTGTCTCTGGCTCCCTCAGCGTGGCTGTGCTCATCTGGCCCTATTTTAGCGGCTGCAC 201
Qy 181 TGCACGCGCAACTACATCCACATGACATGTTCTCTGTCTGTATGTGCGCGCGGAGC 240
Db 202 TGCACGCGCAACTACATCCACATGACATGTTCTCTGTCTGTATGTGCGCGCGGAGC 261
Qy 241 ATCTTGTGAAGACGCTGTCTACTCTGTGCTTCAAGCTGATGAGCGCGGCGCTC 300
Db 262 ATCTTGTGAAGACGCTGTCTACTCTGTGCGCGCACGCTTGTATGAGGCTGAGCGGCTC 321
Qy 301 ACAGAGAGAGTTGCACATCATCGCGGAGGTGCCACCTCCGCGCGCGCTGCCGCGTA 360
Db 322 ACCGAGAGAGTGTGCGGCTATCGCCAGGCGCGCGCGCTGCCACCGCGCTGCC 381
Qy 361 GGCTAGCTGGCTGCCGCGTGGCGTGAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 420
Db 382 GGCTAGCGGCTGTGAGGCTGTGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 441
Qy 421 TACTGATCTGTGAGGCGGCTGTACTTGCACAGCTCATCTTCTGCTGCTTCTCTCTCA 480
Db 442 TACTGATCTGTGAGGCGGCTGTACTTGCACAGCTCATCTTCTGCTGCTTCTCTCTCA 501
Qy 481 GAGAAGAGTACCTGTGGGCTTTCACATCTTTTGGCTGGGCTTACCGGCTGTCTCTGTG 540
Db 502 GAGAAGAGTACCTGTGGGCTTTCACATCTTTGCGCTGGGCTGTCTCTCTGTCTCTGTG 561
Qy 541 GCTGTGTGGTGTGTCAGAGCAAGCTTGGGCAAGCTTGGGCTGTGGGATGTGAGTCTC 600
Db 562 GCTGTGTGGTGTGTCAGAGCAAGCTTGGGCAAGCTTGGGCTGTGGGATGTGAGTCTC 621
Qy 601 GGGCAAGAGTGGATCATCCAGGTGCCATCTGTCATCTGTGCTGCTCAACTTCATC 660
Db 622 GGGCAAGAGTGGATCATCCAGGTGCCATCTGTCATCTGTGCTGCTCAACTTCATC 681
Qy 661 CTTTTATCAACATCATCTGGGCTGTGCTTGCACATCTTGGGAGACCAATGCGGCGCGG 720
Db 682 CTCTTATCAATATGTCTGGGCTGTGCTGCAAGCTTGGGAGACCAACGCGCGCGG 741
Qy 721 TGTGACACAGGAGCAGTACCGGAGCTGTCTAGGTTCACAGTGTGCTGTGCTGCGGCTC 780
Db 742 TGCACACACGCGCAGTACCGGAGCTGTCTCAAAATCGACGCTGTGCTCATGCGGCTC 801
Qy 781 TTTTGTGTGACATACCGGCTTCTGCGCTTCCGCTTACACCGAGGCTCTCAGGAGCATTG 840
Db 802 TTTTGTGTGACATACCGGCTTCTGCGCTTCCATGCGGCGCACCATACCGAGGCTCTCAGGAGCATTG 861

Db 601 CTGCCCAACACCGGGTCTGGGACTTCAGCTTCGGGAACAAAAGTGGATCATCCAGGTG 660
Qy 628 CCATCTCTGGCAATCTGTGTCTCAACTTCATCTCTTTTATCAACATCATCCGGGTCTT 687
Db 661 CCATCTCTGGCTCCATTTGTCTCAACTTCATCTCTTTTATCAACATCATCCGGGTCTC 720
Qy 688 GCCACTAAGCTTTCGGGAGACCAATGCGGGCGGTGTGACACACGAGGACGAGTACCGGAAG 747
Db 721 GCCACCAAGCTTCGGGAGACCAACGCGCGCGGTGTGACACACGAGGACGAGTACCGGAAG 780
Qy 748 CTGCTCAGGTCACAGTTGGTGTCTCGTCCGCTCTTTTGGTGTGCACTACACCGTCTTCATG 807
Db 781 CTGCTCAATCCACGCTGTGTCTCATGCCCTCTTTGGCGTCCACTACATTTGTTTCATG 840
Qy 808 GCCTTGGCGGTACACCGAGGTCTCAGGACATTTGGGAGATTCAGATGCATTTATGAGATG 867
Db 841 GCCACACATACACCGAGGTCTCAGGAGCGCTCTGGCAAGTCCAGATGCATATGAGATG 900
Qy 868 CTCTTCAACTCTTCCAGGATTTTGTGCAATCATATCTGTTTCTCAATGGTGAG 927
Db 901 CTCTTCAACTCTTCCAGGATTTTGTGCAATCATATCTGTTTCTCAATGGTGAG 960
Qy 928 GTGCAGGACAGATTTAGGAAGTCAATGGAGCGGTGTGACACTGGCGTTGGACTTCAAGCGC 987
Db 961 GTACAAGCTGAGATCAAGAAATCTTGGAGCGCTGGACACTGGCACTGGACTTCAAGCGA 1020
Qy 988 AAGCAGCAAGTGGAGTAGCAGTACAGTATATGGCCCAATGTGTCTTCAACAGATGTG 1047
Db 1021 AAGCAGCAGCAGCGGAGCAGCAGTATAGTATACGCGCCCATGTGTGTCCACACAAAGTGTG 1080
Qy 1048 ACCAATGTGGSCCGCTGACAGGACTCAGCTCCCTCCCTCAGCCCCGCG--CTGCGCTCT 1104
Db 1081 ACCAATGTGGSCCGCTGACAGGACTCAGCTCCCTCCCTCAGCCCCGCGCTACTGCCCACT 1140
Qy 1105 GCCACTACCAATGGCCACTCCAGCTGCTGGCCATGCCAAGCAGGAGGCTCCAGCCACT 1164
Db 1141 GCCACCAACGACGCGCCCTCAGCTGCCTGGCCATGCCAAGCAGGAGCAGCCAGCCCTG 1200
Qy 1165 GAGAC---TGAAACCTTACAGTCACTATGGCGGTTCGCAAGGACGATGGATTCCTTAAC 1221
Db 1201 GAGACCTCTCAGAGACACACCACTTGCCTGCTCTCCCAAGGACGATGGGTCTCTCAAC 1260
Qy 1222 GGCTCTCTCAGAGCTTGGATGAGGAGCGCTTCGGGTCTGGCGGCGCTCCATCTGTTG 1281
Db 1261 GGCTCTCTCAGAGCTTGGATGAGGAGCGCTTCGGGTCTGGCGGCGCTCCATCTGTTG 1320
Qy 1282 CAGGAAGGATGGGAACAGTCACTGTGACTGGGCACTAGG 1320
Db 1321 CAGGAAGTGGGAGACAGTCACTGTGACCAGGCGCTGGG 1359

RESULT 11
AAA51737
ID AAA51737 standard; DNA; 1380 BP.
XX AC AAA51737;
XX 31-OCT-2000 (first entry)
XX Human tethered PTH-1 receptor, Tether-R11, coding sequence.
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; tether-R11; osteoporosis; ss.
XX Homo sapiens.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
FT 1..1353
CDS /*tag= a
/product= "Tether-R11"

PN WO200039278-A2.
XX 06-JUL-2000.
PF 30-DEC-1999; 99WO-US031108.
XX 31-DEC-1998; 98US-0114577P.
XX (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
DR P-PSDB; AAY96988.
XX New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
FT treating mammalian conditions characterized by decreases in bone mass.
XX Example 4; Fig 19; 119pp; English.
XX Compounds of the structure or formula S-(L)-n-B, R1-S-(L)-n-R or S-(L)-n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether activity, increasing CAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
SQ Sequence 1380 BP; 245 A; 461 C; 388 G; 286 T; 0 U; 0 Other;
Query Match 74.2%; Score 979.4; DB 3; Length 1380;
Best Local Similarity 84.5%; Pred. No. 7.4e-246;
Matches 1154; Conservative 0; Mismatches 166; Indels 45; Gaps 3;
Qy 1 ATGGGGGCGCGCCGAGTCGACCCAGCTGGCGCTCTACTCTGCTGCCAGTGTCTCAGC 60
Db 1 ATGGGGACCGCGCGAGTCGACCCGCGCTGGCGCTCTCTGCTGCTGCCGCTCAGC 60
Qy 61 TCCGCATATGCGCTG-----GAGGTA 81
Db 61 TCCGCGTACCGGTTTCCGAAATCCAGTGTGATGATGATGCGGGGAGGAGGAGGTG 120
Qy 82 TTTGACCGCTTAGGCGATGATCTACACGCTGGGATCTTCCATGCTCTCTGCGCTCCCTCAG 141
Db 121 TTTGACCGCTTAGGCGATGATTTACACGCTGGGCTACTCTCGTGTCTCTGCGCTCACC 180
Qy 142 GTGGCTGTGCTCATCTCTGGCTATTTAGCGGCTGCTGCTGACGCGCACTACATCCAC 201
Db 181 GTAGCTGTGCTCATCTCTGGCTACTTTAGCGGCTGCTGCTGACGCGCACTACATCCAC 240
Qy 202 ATCCACATGTTCTGCTGTTTATGCTGCGCGCGCGAGCATCTTCTGTAAGGACGCTGTG 261
Db 241 ATGACCTGTTCTGCTGCTTCACTGCTGCGCGCGCTGAGCATCTTCTGTAAGGACGCTGTG 300
Qy 262 CTCTACTCTGGCTTCAAGCTTGGATGAGCGCGCGCTCTCACAGAGGAAGATTGCAATC 321
Db 301 CTCTACTCTGGCGCCACGCTTGTATGAGGCTGAGCGCTCACCAGGAGGAGCTGCGCGCC 360
Qy 322 ATCGCGGAGTGCACCTCTCGCGCGCGCTGCGCGCTAGGCTAGCTGCGCTGCGCGGTG 381
Db 361 ATCGCGGAGGCGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGGTG 420

Db 181 TGACGGCGCACTACATCCATGCAATGCTTCTGCTTTATGCTGCGCGCGGAGC 240
Qy 241 ATCTTCGTGAAGACGCTGTGCTTACTCTGGCTTCACTGATGAGCGCGGCTC 300
Db 241 ATCTTCGTGAAGACGCTGTGCTTACTCTGGCTTCACTGATGAGCGCGGCTC 300
Qy 301 ACAGAGAAAGTTGACATCATCGCGAGGTGCTGCTGCGCGCGGCTGCGCGGTA 360
Db 301 ACAGAGAAAGTTGACATCATCGCGAGGTGCTGCTGCGCGCGGCTGCGCGGTA 360
Qy 361 GGCTACGCTGGCTGCGCGGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 GGCTACGCTGGCTGCGCGGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Qy 421 TACTGATCTGCTGAGGGGCTGCTGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 TACTGATCTGCTGAGGGGCTGCTGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 GAGNAGAGTACCTGCTGGGCTTCAACCATCTTTGGCTGGGCTTACCGGCTGCTTCTG 540
Db 481 GAGNAGAGTACCTGCTGGGCTTCAACCATCTTTGGCTGGGCTTACCGGCTGCTTCTG 540
Qy 541 GCTGTGGGTGCTGCTGAGCAACCTTGGCCAACTGCGGCTGCTGCGGATCTGAGCTCC 600
Db 541 GCTGTGGGTGCTGCTGAGCAACCTTGGCCAACTGCGGCTGCTGCGGATCTGAGCTCC 600
Qy 601 GGGCACAAGAGTGGATCATCCAGGTGCCATCTGTCGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 GGGCACAAGAGTGGATCATCCAGGTGCCATCTGTCGCTGCTGCTGCTGCTGCTGCTG 660
Qy 661 CTTTATATCAACATCATCCGGTCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 CTTTATATCAACATCATCCGGTCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Qy 721 TGTGACACAGGAGGAGTACCGAAGCTGCTGAGGTCCAGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 TGTGACACAGGAGGAGTACCGAAGCTGCTGAGGTCCAGCTGCTGCTGCTGCTGCTGCTG 780
Qy 781 TTTGCTGTGCACTACACCGCTTTCATGCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 TTTGCTGTGCACTACACCGCTTTCATGCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 841 TGGCAGATCCAGATGCAATGATGATGCTTCACTGCTTCACTGCTTCACTGCTTCACTG 900
Db 841 TGGCAGATCCAGATGCAATGATGATGCTTCACTGCTTCACTGCTTCACTGCTTCACTG 900
Qy 901 ATCATATCTGTTTCTGCAATGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 960
Db 901 ATCATATCTGTTTCTGCAATGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 960
Qy 961 TGGACACTGGCGTTG 975
Db 961 TGGACACTGGCGTAG 975

RESULT 13
ID AB242719 standard; DNA; 1948 BP.
XX AC AB242719;
XX DT 04-MAR-2003 (first entry)
XX DE Human parathyroid hormone receptor 1 nucleotide SEQ ID NO:228.
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer; gene; ds.
XX Homo sapiens.
XX WO200261087-A2.
XX 08-AUG-2002.
XX 19-DEC-2001; 2001WO-US050107.
XX 19-DEC-2000; 2000US-0257144P.
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX Burmer GC, Roush CL, Brown JP;
XX WPI; 2003-046718/04.
XX P-PSDB; ABP81872.
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
XX Disclosure; Fig 1; 523pp; English.
XX The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (I) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX exemplification of the present invention
XX SQ Sequence 1948 BP; 405 A; 600 C; 570 G; 373 T; 0 U; 0 Other;

Query Match 73.2%; Score 966.8; DB 8; Length 1948;
Best Local Similarity 86.6%; Pred. No. 1.7e-242;
Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2;
Qy 69 TGGCGCTGGAGGTATTTGACCGCTAGGCATGATCTACCGCTGGGATCTCCATGTCTCT 128
Db 565 TGAACGGAGGTGTTTACCGCTGGCATGATTTACCGCTGGGCTACTCTCGGTGCTCT 624
Qy 129 CGCTCCCTCACGGTGGCTGTGCTCATCTCTGGCTATTTTAGCGGCTGCATCGACGCG 188
Db 625 GGGCTCCCTCACCGTAGTGTCTCATCTCTGGCTACTTTTAGCGGCTGCACTCGACGCG 684
Qy 189 CAATCATATCCATGACATGTTCTGCTGTTTATGCTGCGGCGCGGAGCATCTTCGT 248
Db 685 CAATCATATCCATGACCTGTTCTGCTCTTCTCATGCTGCTGCGCGGTGAGCATCTTCGT 744

249 GAAGGACGCTGTGCTTACTTCTGCTTCA CGCTGGATGAGGCGAGCGCTTACAGAGGA 308
Db |||||
745 CAAGGACGCTGTGCTTACTTCTGCGCCACGCTTTGATGAGGCTGAGCGCTTACCGAGGA 804
Qy |||||
309 AGAGTTCACATCATCGGAGGTGCGACCTCCGCGCGCGCTGCGCGGTAGGCTACGC 368
Db |||||
805 GGAGCTGGCGCCATCGCCAGGCGCCCGCGCGCTGCGCACCGCGCGCTGCGCGCTACGC 864
Qy |||||
369 TGGCTGCGCGGTGCGGCTGCTTCTTCTCTACTTCTGCTTACCAACTACTACTGAT 428
Db |||||
865 GGGCTGCGAGGCTGTGACCTTCTTCTTCTTACTTCTGSCCACTACTACTACTGAT 924
Qy |||||
429 CTTGCTGAGGGCTGTACTTGCACAGCTCATCTTATGCGCTTTTCTCAGAGAAGAA 488
Db |||||
925 TCTGCTGAGGGCTGTACTTGCACAGCTCATCTTATGCGCTTCTTCTCAGAGAAGAA 984
Qy |||||
489 GTACTCTGCGGCTTCAACCTTTGCTGGGTCTACCGCTCTCTTCTGCTGGCTGTG 548
Db |||||
985 GTACTCTGCGGCTTCAAGCTTCTGCGGTGGGTCTGCGCGCTCTCTTCTGCTGGCTGTG 1044
Qy |||||
549 GGTGCTGTTCAGAGCAACCTTTGGCCAACTTGGGTGCTTGGGATCTGAGCTCCGCGCACAA 608
Db |||||
1045 GGTGCTGTTCAGAGCTTCTGCTGGCCAACTTGGGTGCTTGGGATCTGAGCTCCGCGCACAA 1104
Qy |||||
609 GAAGTGATCATCAGGTGCCATCTCTGGCACTTGTGTGCTCAACTTCTTCTTTTAT 668
Db |||||
1105 AAAGTGATCATCAGGTGCCATCTCTGGCTTCCATTTGTCTCACTTCTTCTTCTTAT 1164
Qy |||||
669 CAACATCATCGGCTGTCTTCACTTCTGCGGAGACCAATCGCGCGGCTGTGACAC 728
Db |||||
1165 CAATATCGTGGGTGTCTGCGCACCAAGCTGCGGAGACCAACCGCGCGGTGTGACAC 1224
Qy |||||
729 CAGGACGAGTACCGGAGCTGTCTGAGTCCAGCTTGTGTCTGCTGCGCTCTTGTGTGT 788
Db |||||
1225 ACGGACGAGTACCGGAGCTGTCTCAATCACTGCTGTCTGCTGCTTGTGCGGT 1284
Qy |||||
789 GCACTACACCGTCTTCACTGCGCTTGGCGTACACCGAGGTCTCAGGACATTTGTGGCAGAT 848
Db |||||
1285 CCATCATATTGCTTCTGCGCACACCATACACGAGGTCTCAGGAGCGCTCTGGCAAGT 1344
Qy |||||
849 CCAGATGATATCAGATGCTTCTCACTCTTCCAGGGATTTTGTGCGCATCATATA 908
Db |||||
1345 CCAGATGATATCAGATGCTTCTCACTCTTCCAGGGATTTTGTGCGCAATCATATA 1404
Qy |||||
909 CTGTTCTGCAATGCTGAGGTGCGGAGGAGTATGAGGATCATGAGCGCGCTGACACT 968
Db |||||
1405 CTGTTCTGCAATGCGGAGGTACAGGTGAGTACAGAAATCTTGGAGCGCGCTGACACT 1464
Qy |||||
969 GCGCTTGGACTTCAAGCGCAAGCAGAGTGGAGTAGCAGCTACAGCTATGCGCCCAAT 1028
Db |||||
1465 GGCAGTGGACTTCAAGCGAAAGGACGCGAGGAGCAGAGCTATAGCTACGCGCCCAT 1524
Qy |||||
1029 GGTGCTTCAACGAGTGTACCAATGTGGGCGCGCGCTGAGGACTCAGCTTCCCGCTCAG 1088
Db |||||
1525 GGTGCTTCAACGAGTGTACCAATGTGGGCGCGCGCTGAGGACTCAGCTTCCCGCTCAG 1584
Qy |||||
1089 CCCCCGCTCTGCTGCTTCAATGCGGAGTCCAGCTGCTGCGGCAATGCCAA 1145
Db |||||
1585 CCCCCGCTCTGCTGCTTCAATGCGGAGTCCAGCTGCTGCGGCAATGCCAA 1644
Qy |||||
1146 GCCAGGGGCTCCAGCCTCAGAC---TGAAACCTTACCACTATGCGGCTTCCCAA 1202
Db |||||
1645 GCCAGGGACCCAGCCTTGGAGACCTTGGAGACCAACACCACTGCGGCTGCTGCCAA 1704
Qy |||||
1203 GGAAGATGATTCCTTAAAGGCTCTGCTGAGGCTGTGATGAGGAGGCTTCCGGGTCTGC 1262
Db |||||
1705 GGACGATGGGTCTCTCAACGCTCTGCTCAGGCTGTGAGCGAGGAGGCTTCTGGGCTGA 1764
Qy |||||
1263 GCGGCGGCTCTCTTGTGAGGAGGATGGGAACAGTATGATGCTGCGGCTAGG 1320
Db |||||
1765 GCGGCGGCTCTCTTGTGAGGAGGATGGGAACAGTATGATGCTGCGGCTAGG 1822

RESULT 14

ACAS6655
ID ACAS6655 standard; cDNA; 1948 BP.

XX AC ACAS6655;

XX 06-JUN-2003 (first entry)

XX Human signalling pathway polynucleotide probe SEQ ID NO 1253.

DE Human; probe; ss; array element; Parkinson's disease;

XX Human; probe; ss; array element; Parkinson's disease;

KW signalling pathway population; cancer; adenocarcinoma; leukaemia;

KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

XX Homo sapiens.

XX US6500938-B1.

XX 31-DEC-2002.

XX 30-JAN-1998; 98US-00016434.

XX 30-JAN-1998; 98US-00016434.

XX (INCY-) INCYTE GENOMICS INC.

XX Au-Young J, Seilhamer JJ;

XX WPI; 2003-352189/33.

XX Combination of polynucleotide probes, useful as array elements in a

PT microarray for monitoring the expression of a number of target

XX polynucleotides.

PS Claim 1; SEQ ID NO 1253; 65pp; English.

CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1

XX Sequence 1948 BP; 405 A; 600 C; 570 G; 373 T; 0 U; 0 Other;

Query Match 73.2%; Score 966.8; DB 10; Length 1948;
Best Local Similarity 86.6%; Pred. No. 1.7e-242;
Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2;

Qy 69 TGGCTGGAGGATTTGACCGGCTTAGCATGATCTACCGTGGGATACCTGCTCTCT 128

Db 565 TGAACGGGAGGTGTTTACCGGCTTACCGGCTTACCGGCTTACCGGCTTACCGGCT 624

Qy 129 CGCTCCCTCACGGTGGCTGTCTCATCTCCGGCTATTTAGGGGCTGCTGCTGCGG 188

Db 625 GGGCTCCCTCACCGTGGCTGTCTCATCTCCGGCTTACTTTAGGGGCTGCTGCTGCGG 684

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Best Local Similarity 99.8%; Pred. No. 0;									
Matches 1245; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
Qy	73	CTGAGGATTTTGAACCGCTAGGATGATATACACCGTGGGATACTCAATGTCTCTCGCC	132						
Db	613	CGGAGGATTTTGAACCGCTAGGATGATATACACCGTGGGATACTCAATGTCTCTCGCC	672						
Qy	133	TCCCTCAGGTGGTGTGCTCATCTCGGCTATTTTAGGGGGTGCACCTGACGCGCAAC	192						
Db	673	TCCCTCAGGTGGTGTGCTCATCTCGGCTATTTTAGGGGGTGCACCTGACGCGCAAC	732						
Qy	193	TACATCACATGACATGTTCTCTGCTTATGCTGCGCGCGGAGCATCTTCTGTAAG	252						
Db	733	TACATCACATGACATGTTCTCTGCTTATGCTGCGCGCGGAGCATCTTCTGTAAG	792						
Qy	253	GACGCTGTCTACTCTGGCTTACGCTGGATGAGCGCGCTCACAGAGGAAGAG	312						
Db	793	GACGCTGTCTACTCTGGCTTACGCTGGATGAGCGCGCTCACAGAGGAAGAG	852						
Qy	313	TTGCACATCATCGCGAGTGCCACCTCCGCGCGCTGCGCGGTAGGCTAGCTGGC	372						
Db	853	TTGCACATCATCGCGAGTGCCACCTCCGCGCGCTGCGCGGTAGGCTAGCTGGC	912						
Qy	373	TGCGCGTGGGGTGACCTTCTCTCTACTTCTGCTACCAACTACTACTGATCCTG	432						
Db	913	TGCGCGTGGGGTGACCTTCTCTCTACTTCTGCTACCAACTACTACTGATCTG	972						
Qy	433	GTGAGGGGCTGTACTTGCACAGCCTCATCTTCATGCGCTTTTCTCAGAGAAATAC	492						
Db	973	GTGAGGGGCTGTACTTGCACAGCCTCATCTTCATGCGCTTTTCTCAGAGAAATAC	1032						
Qy	493	CTGTGGGGCTTACACATCTTGGCTGGGTCTACCGGCTCTTCTGCTGTGTGGTC	552						
Db	1033	CTGTGGGGCTTACACATCTTGGCTGGGTCTACCGGCTCTTCTGCTGTGTGGTC	1092						
Qy	553	GGTGTACAGCAACTTGGCCAACTGGGTGCTGGGATCTAGCTCGGGCAACAAG	612						
Db	1093	GGTGTACAGCAACTTGGCCAACTGGGTGCTGGGATCTAGCTCGGGCAACAAG	1152						
Qy	613	TGATCATCCAGGTGCCATCTGGCATCTGTTGTGCTCAACTTTTATCAAC	672						
Db	1153	TGATCATCCAGGTGCCATCTGGCATCTGTTGTGCTCAACTTTTATCAAC	1212						
Qy	673	ATCATCCGGGTCTTGCACACTAAGCTTCGGAGACCAATGCGGCGGTGACACAGG	732						
Db	1213	ATCATCCGGGTCTTGCACACTAAGCTTCGGAGACCAATGCGGCGGTGACACAGG	1272						
Qy	733	CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGTCTGTCGCGCTTTTGGTGTGAC	792						
Db	1273	CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGTCTGTCGCGCTTTTGGTGTGAC	1332						
Qy	793	TACACCGTCTTTCATGGCTTCCGTATACACCGGTCTCAGGGAATTTGGGACATCCAG	852						
Db	1333	TACACCGTCTTTCATGGCTTCCGTATACACCGGTCTCAGGGAATTTGGGACATCCAG	1392						
Qy	853	ATGCATTTATGATGCTCTTCAACTCTTCCAGGATTTTGTGTCATCATATCTGT	912						
Db	1393	ATGCATTTATGATGCTCTTCAACTCTTCCAGGATTTTGTGTCATCATATCTGT	1452						
Qy	913	TTCTGCAATGTGAGGTGACGACAGATTTAGGAAGTCATGGAGCGCTGGACACTGGCG	972						
Db	1453	TTCTGCAATGTGAGGTGACGACAGATTTAGGAAGTCATGGAGCGCTGGACACTGGCG	1512						
Qy	973	TTGACCTTCAAGCGCAAGACGAAAGTGGGAGTACAGCTACAGCTATGGCCCAATGGTG	1032						
Db	1513	TTGACCTTCAAGCGCAAGACGAAAGTGGGAGTACAGCTACAGCTATGGCCCAATGGTG	1572						
Qy	1033	TCTCACAGGTGTGACCAATGTGGGCCCGCTGCAGACTCAGCTCCCTCAGCCCC	1092						
Db	1573	TCTCACAGGTGTGACCAATGTGGGCCCGCTGCAGACTCAGCTCCCTCAGCCCC	1632						
Qy	1093	CGCTTGCCTCTGTCACCTACCAATGTGGCCACTCCAGCTGCTGGCCATGCGCAAGCCAGGG	1152						

Db	1633	CGCCTGCCTCCTGCCACTACCAATGGCCACTCCACAGCTGCCTGGCCATGCAAGCCAGGG	1692						
Qy	1153	GCTCCAGCCACTGAGACTGAAACCTTACAGTCACTATGGCGTTCCTCAGGACGATGGA	1212						
Db	1693	GCTCCAGCCACTGAGACTGAAACCTTACAGTCACTATGGCGTTCCTCAGGACGATGGA	1752						
Qy	1213	TTCTTTAAACGGCTCCTGCTCAGGCTTGGATAGGAGGCTTCCGGGTCTGCGCGCGCCCT	1272						
Db	1753	TTCTTTAAACGGCTCCTGCTCAGGCTTGGATAGGAGGCTTCCGGGTCTGCGCGCGCCCT	1812						
Qy	1273	CCATTGTTGAGGAAGATGGGAAAACAGTCACTGATGGGCACTAGG	1320						
Db	1813	CCATTGTTGAGGAAGATGGGAAAACAGTCACTGATGGGCACTAGG	1860						
RESULT 2									
US-08-468-249A-3									
; Sequence 3, Application US/08468249A									
; Patent No. 5886148									
; GENERAL INFORMATION:									
; APPLICANT: Segre et al., Gino V.									
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA									
; TITLE OF INVENTION: ENCODING SAME									
; NUMBER OF SEQUENCES: 21									
; CORRESPONDENCE ADDRESS:									
; ADDRESSEE: Fish & Richardson P.C.									
; STREET: 225 Franklin Street									
; CITY: Boston									
; STATE: MA									
; COUNTRY: USA									
; ZIP: 02110-2804									
; COMPUTER READABLE FORM:									
; MEDIUM TYPE: Floppy disk									
; COMPUTER: IBM PC compatible									
; OPERATING SYSTEM: PC-DOS/MS-DOS									
; SOFTWARE: Patent In Release #1.0, Version #1.30									
; CURRENT APPLICATION DATA:									
; APPLICATION NUMBER: US/08/468,249A									
; FILING DATE: 06-JUN-1995									
; CLASSIFICATION: 530									
; PRIOR APPLICATION DATA:									
; APPLICATION NUMBER: US 07/864,475									
; FILING DATE: 06-APR-1992									
; PRIOR APPLICATION DATA:									
; APPLICATION NUMBER: US 07/681,702									
; FILING DATE: 04-MAY-1991									
; ATTORNEY/AGENT INFORMATION:									
; NAME: Fraser, Janis K.									
; REGISTRATION NUMBER: 34,819									
; REFERENCE/DOCKET NUMBER: 00786/071003									
; TELECOMMUNICATION INFORMATION:									
; TELEPHONE: 617/542-5070									
; TELEFAX: 617/542-8906									
; INFORMATION FOR SEQ ID NO: 3:									
; SEQUENCE CHARACTERISTICS:									
; LENGTH: 2051 base pairs									
; TYPE: nucleic acid									
; STRANDEDNESS: single									
; TOPOLOGY: linear									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: 73..1846									
US-08-468-249A-3									
Query Match 94.2%; Score 1243.2; DB 2; Length 2051;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 1245; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
Qy	73	CTGAGGATTTTGAACCGCTAGGATGATATACACCGTGGGATACTCAATGTCTCTCGCC	132						
Db	613	CGGAGGATTTTGAACCGCTAGGATGATATACACCGTGGGATACTCAATGTCTCTCGCC	672						
Qy	133	CTGAGGATTTTGAACCGCTAGGATGATATACACCGTGGGATACTCAATGTCTCTCGCC	1272						
Db	613	CGGAGGATTTTGAACCGCTAGGATGATATACACCGTGGGATACTCAATGTCTCTCGCC	672						
Qy	133	TCCTCAGGTGGTGTGCTCATCTCGGCTATTTTAGGGGGTGCACCTGACGCGCAAC	192						

Db 745 CAAGGACGCTGTGCTCTACTCTGGCGCCACGCTTTGATGAGGCTGAGCGCTCACCGGAGGA 804
Qy 309 AGAGTTGCACATCATCGCGGAGGTGCCACCTCCCGCGCGCGCTGCCCGTAGCTACGC 368
Db 805 GGAGCTGCGGCCCATCGGCCAGGCGCCCGCGCGCTGCCACCGCGCTGCCCGCTACGC 864
Qy 369 TGGCTGCCCGCTGGCGGTGACCTTCTTCTCTACTTCTTGCTAGCTACCAACTACTACTGGAT 428
Db 865 GGGCTGCAGGGTGGCTGTGACCTTCTTCTTACTTCTTGCGCACCAACTACTACTGGAT 924
Qy 429 CCTGGTGAGGGGCTGTACTTTCAGCAGCCTCATCTTTCATGGCCCTTTTCTCAGAGAAGAA 488
Db 925 TCTGGTGAGGGGCTGTACTTTCAGCAGCCTCATCTTTCATGGCCCTTCTTCTCAGAGAAGAA 984
Qy 489 GTACTGTGGGGCTTACCATCTTTTGGGTGGGGTCTACCGGCTGTCTTCTGGGTGTGTG 548
Db 985 GTACTGTGGGGCTTACAGTCTTTCGGGTGGGGTCTGCGCGCTGTCTTCTGGGTGTGTG 1044
Qy 549 GGTGGTGTGAGAGCAACCTTGGGCCAACACTGGGGTGTGGGATCTGAGCTCCGGGACAA 608
Db 1045 GGTGAGTGTGAGAGTACCTTGGGCCAACACCGGGTGTGGGATCTGAGCTCCGGGACAA 1104
Qy 609 GAAGTGGATCATCAGGTGCCCATCTCTGGCATCTGTGTGTCTCAACTTCATCTCTTTTAT 668
Db 1105 AAAGTGGATCATCAGGTGCCCATCTCTGGCATCTGTGTGTCTCAACTTCATCTCTTTTAT 1164
Qy 669 CAACATCATCGGGTGTCTTGCATTAAGCTTCCGGAGACCAATCGCGCGGGTGTGAC 728
Db 1165 CAATATCTCGGGTGTCTCGCCACCAAGCTCGCGGAGACCAACCGCGCGGGTGTGAC 1224
Qy 729 CAGCAGCAGTACCGGAGCTGTCTCAGTCCACCTTGGTGTCTGTGGCGCTCTTTGGTGT 788
Db 1225 ACGCAGCAGTACCGGAGCTGTCTCAATCACACCTGTGTCTCAATGCCCCCTCTTTGGCGT 1284
Qy 789 GCACTACACCGCTTTCATGGCTTTGCCGTACACCGAGTCTTCAGGAGCAATTTGGGACAGAT 848
Db 1285 CCACATATTGTCTTTCATGGCCACACCATACACCGAGTCTTCAGGAGCGTCTTCGCAAGT 1344
Qy 849 CCAGATGATTATGAGATGTCTTCAACTCTCTTCAGGAGATTTTGTGGCATCATATA 908
Db 1345 CCAGATGACATATGAGATGTCTTCAACTCTCTTCAGGAGATTTTGTGGCAATCATATA 1404
Qy 909 CTGTTTCTGCAATGTGAGGTGAGGAGCAGGATTTAGGAAGTCATGGAGCGCTGGACACT 968
Db 1405 CTGTTTCTGCAATGTGAGGTGAGGAGCAGGATTTAGGAAGTCATGGAGCGCTGGACACT 1464
Qy 969 GGCCTTGGACTTCAAGCGCAAGCAGCAAGTGGAGTAGCAGCTACAGCTATGGCCCAAT 1028
Db 1465 GGCCTTGGACTTCAAGCGCAAGCAGCAGCGGAGCAGCAGCTATAGCTACGGCCCAT 1524
Qy 1029 GGTGTCTCAGCAGGTGTGACCAATGTGGGCCCCCGGTGAGGACTCAGCCTCCCGCTCAG 1088
Db 1525 GGTGTCCACACAAGTGTGACCAATGTGGGCCCCCGGTGAGGACTCAGCCTCCCGCTCAG 1584
Qy 1089 CCCCCTGCTCTGCACTTACCAATGGCCACTTCCAGCTGCTCCAGCATGCGCAATGCCAA 1145
Db 1585 CCCCCTGCTCTGCACTTACCAATGGCCACTTCCAGCTGCTCCAGCATGCGCAATGCCAA 1644
Qy 1146 GCCAGGGGCTCCAGCCTATGAGC---TGAAACCTTACCAAGTCACTATGGCGGTCCCAA 1202
Db 1645 GCCAGGGACCCAGCCTGGAGACCTTCGAGACCAACCACTTCCATGGCTGCTCCCAA 1704
Qy 1203 GGAAGATGATTCCTTAACGGCTCTGTCTAGGCTGTGATGAGGAGCGCTCCGGGTCTGC 1262
Db 1705 GGAAGATGATTCCTTAACGGCTCTGTCTAGGCTGTGATGAGGAGCGCTCCGGGTCTGA 1764
Qy 1263 GCGCGCGCTCCATTTGTTGAGGAAGGATGGAAACAGTCTATGTGACTTGGGCACTAGG 1320
Db 1765 GCGCGCACCTGCCCTGTCTAGGAAGAGTGGGAGACAGTCTATGTGACAGGCGCTGGG 1822

RESULT 4

US-07-864-475A-4

; Sequence 4, Application US/07864475A
; Patent No. 5494806
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, John T. [Jr.]
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
; TITLE OF INVENTION: AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864,475A
; FILING DATE: 04-06-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/681,702
; FILING DATE: 05-04-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/071002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELETYPE: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2010
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-07-864-475A-4

Query Match 73.1%; Score 965.2; DB 1; Length 2010;
Best Local Similarity 86.6%; Pred. No. 5.9e-256;
Matches 1089; Conservative 0; Mismatches 163; Indels 6; Gaps 2;
Qy 69 TGGCTGAGGATTTTGAACCGCTAGGCATGATCTACACCGTGGGATCTCCATGTCTCT 128
Db 564 TGAACGGGAGGTCTTTGACCGCTTGGGCATGATTACCGTGGGCTACTCTCGTGTCCCT 623
Qy 129 CGCTCCCTCACGCTGGCTGTCTATCTCGGCTATTTTAGCGGCTGCACGTGACGCG 188
Db 624 GGGTCCCTCACGCTAGTGTCTATCTTGGCTACTTTAGGCGGTGACCTTGACGCG 683
Qy 189 CAATACATCCACATGACATGTTCTGTCTTATGTCTGCGCGCGGAGCATCTTCTGT 248
Db 684 CAATACATCCACATGACCTGTTCTGTCTTCTGCTGCTGCGCGGTGAGCATCTTCTGT 743
Qy 249 GAAGGAGCTGTCTCTACTCTGGCTTACGCTGGATGAGGCGGAGGCTTACAGAGGA 308
Db 744 CAAGGAGCTGTCTCTACTCTGCGCCACGCTTGTATGAGGCTGAGGCGCTTACCGAGGA 803
Qy 309 AGAGTTGCACATCATCGCAGGTGCCACCTCCGCGCGCGCTGCGCGCTAGGCTACGC 368
Db 804 GAGCTGCGCGCATCGCCAGGCGCCCGCGCTGCGCACCGCGCTGCGCGCTAGGCTACGC 863
Qy 369 TGGCTGCGCGTGGCGGTGACCTTCTTCTCTTACTTCTTGGCTACCAACTACTACTGGAT 428

Db 864 GGGCTGCAGGGTGGCTGTGACCTTCTCTCTTACTTCTTGGCCACCACTACTACTCGAT 923
Qy 429 CCTGGTGGAGGGGTGTACTTTGACAGCCTCATCTTATGGCCCTTTTCTCAGAGAAGAA 488
Db 924 TCTGGTGGAGGGGTGTACTTGCAGCAGCCTCATCTTCAATGGCCCTTCTTCTCAGAGAAGAA 983
Qy 489 GTACTGTGGGGCTTACCATCTTTGGCTGGGGTCTACCGGCTGTCTTGGCTGTGTG 548
Db 984 GTACTGTGGGGCTTACCATCTTTGGCTGGGGTCTGCGCGCTGTCTTGGCTGTGTG 1043
Qy 549 GGTGGTGTGACAGCAACTTGGCCCAACACATGGGTGTGGGATCTGAGCTCCGGGCACAA 608
Db 1044 GGTGAGTGTGAGAGTACCTTGGCCCAACACCGGGTGTGGGATCTGAGCTCCGGGACAA 1103
Qy 609 GAAGTGGATCATCAGAGTGGCCATCTTGGGATCTTGTGTCAACTTCATCTTTTAT 668
Db 1104 AAAGTGGATCATCAGAGTGGCCATCTTGGGCTCCATTTGTCTCAACTTCATCTTTAT 1163
Qy 669 CAACATCATCCGGGTGTGTGACATAGCTTGGGAGACCAATGGGGCGGGTGTGACAC 728
Db 1164 CAATATCTCCGGGTGTGTGACATAGCTTGGGAGACCAATGGGGCGGGTGTGACAC 1223
Qy 729 CAGCAGCAGTACCGGAGCTGTGAGTCCACGTTGGTGTCTGCTGCGCTCTTTGGTGT 788
Db 1224 ACGCAGCAGTACCGGAGCTGTGAGTCCACGTTGGTGTCTGCTGCGCTCTTTGGTGT 1283
Qy 789 GCACTACACCGCTTTCATGGCTTTCGCGTACACGAGGTCTCAGGGACATTTGGGAGAT 848
Db 1284 CCATCATATTGTCTTATGGCCACACCATACACGAGGTCTCAGGGACGCTTGGCAGT 1343
Qy 849 CCAGATGATATGAGATGTCTTCAACTCTTCCAGGAGTATTTTGTGGCATCATATA 908
Db 1344 CCAGATGATATGAGATGTCTTCAACTCTTCCAGGAGTATTTTGTGGCATCATATA 1403
Qy 909 CTGTTTCTGCAATGGTGTGAGGTGACGAGATTTAGGAGTCTAGGAGCGCTGGACACT 968
Db 1404 CTGTTTCTGCAATGGGAGGTGACGAGTGTAGATCAAGAAATCTTGGAGCGCTGGACACT 1463
Qy 969 GGGCTGGAGCTTCAAGCGCAAGCAGAGTGGGAGTACAGCTATGAGCGCCCAAT 1028
Db 1464 GGCATGAGCTTCAAGCGCAAGCAGAGTGGGAGTACAGCTATGAGCGCCCAAT 1523
Qy 1029 GGTGTCTACAGAGTGTGACCAATGTGGGCCCCGCTGAGGACTCAGCTTCCCTCTAG 1088
Db 1524 GGTGTCTACAGAGTGTGACCAATGTGGGCCCCGCTGAGGACTCAGCTTCCCTCTAG 1583
Qy 1089 CCCCCGCTTCTGCAATGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 1145
Db 1584 CCCCCGCTTCTGCAATGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAG 1643
Qy 1146 GCCAGGGGCTCAGCGCACTGAGAC---TGAAACCTTACCACTACTATGGCGGTTCGCAA 1202
Db 1644 GCCAGGAGCCCGCTGAGAGCCCTGAGACACACACCTGCTGAGTGGCTTCCCAA 1703
Qy 1203 GGACGATGATTCCTTAAAGGCTCTGCTCAGGCTTGGATGAGGAGGCTTCCGGGTCTGC 1262
Db 1704 GGACGATGATTCCTTAAAGGCTCTGCTCAGGCTTGGATGAGGAGGCTTCCGGGTCTGC 1763
Qy 1263 GCGGCGGCTCCATTTGAGGAGGAGTGGGAGGAGTGTGAGTGGGAGTGGGAGTGGGAG 1320
Db 1764 GCGGCGGCTCCATTTGAGGAGGAGTGGGAGGAGTGTGAGTGGGAGTGGGAGTGGGAG 1821

RESULT 5

US-08-468-249A-4
; Sequence 4, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,249A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/071003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2010 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 28..1807
US-08-468-249A-4

Query Match 73.1%; Score 965.2; DB 2; Length 2010;
Best Local Similarity 86.6%; Pred. No. 5.9e-256;
Matches 1089; Conservative 0; Mismatches 163; Indels 6; Gaps 2;

Qy 69 TGGCTGGAGGATTTGACCGCTTAGCATGATCTACCGTGGGAGTACTCCTGCTCT 128
Db 564 TGAACGGAGGTGTTGACCGCTGGCATGATTTACACCGTGGGCTACTCCGTGTCCT 623
Qy 129 CGCTCCCTCAGGTGGTGTCTCATCTGGGCTATTTAGGGGCTGCACTGCACGG 188
Db 624 GGGTCCCTCAGGTGGTGTCTCATCTGGGCTACTTTAGGGGCTGCACTGCACGG 683
Qy 189 CAATCATCATCCATGCATGTTCTGTTTATGCTGCGCGCGGAGCATCTTCTGT 248
Db 684 CAATCATCATCCATGCATGTTCTGTTTATGCTGCGCGCGGAGCATCTTCTGT 743
Qy 249 GAAGGAGCTGTGCTCTACTCTGGCTTACGCTGGAGTGGGCGGAGCGCTCAGAGGA 308
Db 744 CAAGGAGCTGTGCTCTACTCTGGCGCACGCTTGTATGAGGCTGAGCGCTCAGAGGA 803
Qy 309 AGAGTTGCACATCATCGGAGGTGGCACTCCGCGCGGCGGCTGCGCGCGGTAGGCTACGC 368
Db 804 GGAGTGGCGGCTCATCGCGCGGCGGCGGCTGCGCGCGGTAGGCTACGC 863
Qy 369 TGGCTCCGCGGTGGGCTGACCTTCTCTCTACTTCTGGCTACCACTACTACTGAT 428
Db 864 GGGCTGAGGGTGGGCTGAGGCTTCTCTCTTACTTCTTCTGGCGGAGCTACTTGGAT 923
Qy 429 CTGGTGGAGGGCTGTACTTTCACAGCCTCATCTTCTCATGGCCCTTTTCTCAGAGAAGAA 488
Db 924 TCTGGTGGAGGGCTGTACTTTCACAGCCTCATCTTCTCATGGCCCTTCTTCTCAGAGAAGAA 983
Qy 489 GTACTGTGGGGCTTCAACCATCTTGGGTGGGTCTACCGGCTGTCTTCTGGCTGTGTG 548

Db 984 GTACCTGGGGCTTACAGTCTTCGGCTGGGGCTGCCCGCTGCTCTTCGTGGCTGTGTG 1043
Qy 549 GGTGGTGTGACAGCAACCTTGGCAACACTGGGTGCTGGGATCTGAGCTCCGGGACAA 608
Db 1044 GGTCAAGTGTGACAGTCACTCCCTGGCCAAACACCGGGTGTGGGACTTGAAGCTCCGGGAA 1103
Qy 609 GAAGTGGATCATCAGAGTGCCCATCTCTGGGATCTGTTGTGCTCAACTTCACTCTTTTAT 668
Db 1104 AAGTGGATCATCAGAGTGCCCATCTGGGCTCACTGTTGCTCAACTTCACTCTTTAT 1163
Qy 669 CAACATCATCGGTGTCTGCACTAAGCTTGGGAGACCAATGCGGGCGGTGTGACAC 728
Db 1164 CAATATCGTCCGGTGTCTGCGCACCAAGACGCGGGAGACCAACGCGCGGGTGTGACAC 1223
Qy 729 CAGCAGAGTACCGGAGCTGCTCAGGTCCAGCTTGGTGTGCTGCTGCTGCTGCTGCTGCT 798
Db 1224 ACGCAGCAGTACCGGAGCTGCTCAATCCACGCTGCTGCTGCTGCTGCTGCTGCTGCT 1283
Qy 789 GCATACACCTGCTTCAATGGCTTGGCGTACACCGAGTCTCAGGGACATTTGGGAGAT 848
Db 1284 CCATACATTTCTTATGGCCACACCATACACCGAGTCTCAGGGAGCTTCTGGCAAGT 1343
Qy 849 CCAGATGCATATCAGATGCTTTCAACTCTTCCAGGGATTTTGTGTCCTATCATATA 908
Db 1344 CCAGATGCATATCAGATGCTTTCAACTCTTCCAGGGATTTTGTGTCCTATCATATA 1403
Qy 909 CTGTTTCTGCAATGCTGAGGTGAGGAGGATAGGAAGTCTGAGGAGCGCTGGACACT 968
Db 1404 CTGTTTCTGCAATGCTGAGGTGAGGAGGATAGGAAGTCTTGGAGCGCTGGACACT 1463
Qy 969 GGCCTTGGACTTCAAGCGCAAGCACGAAGTGGGAGTAGCAGCTACAGCTATGGCCCAAT 1028
Db 1464 GGCATGGACTTCAAGCGAAGGACGACGCGGAGGAGCAGAGCTATAGCTACGGCCCAT 1523
Qy 1029 GGTGCTCACAGAGTGTGACCAATGTGGGCCCCCTGTCAGGACTCAGCTCCCGCTCAG 1088
Db 1524 GGTGTCCACAAAGTGTGACCAATGTGGGCCCCCTGTCAGGACTCAGCTCCCGCTCAG 1583
Qy 1089 CCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1145
Db 1584 CCCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1643
Qy 1146 GCGAGGCTCCAGCCTAGAC---TGAACCTTACCAGTCACTATGGCGTTCCTCAA 1202
Db 1644 GCGAGGACCCAGCCTGAGACCTTGCAGACCAACCTGCTGCTGCTGCTGCTGCTGCTGCT 1703
Qy 1203 GCGAGTGGATTCCTTAAAGCTCTCTGCTCAGGCTTGAATGAGGAGCCTCCGGGTCTGC 1262
Db 1704 GCGAGTGGGTTCCTCAAGGCTCTGCTCAGGCTTGAATGAGGAGCCTCTGGGCTGTA 1763
Qy 1263 GCGGCGCTCCATGTTGAGGAGGATGGGAACAGTCACTGAGTGGGCACTAGG 1320
Db 1764 GCGGCGCTCCCTGCTTACAGGAAGTGGGAGACGACTCATGTGACAGGCGCTGGG 1821

RESULT 6

US-09-826-509-562
; Sequence 562, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIORITY FILING DATE: 2001-04-05
; PRIORITY FILING DATE: 60/195,747
; PRIORITY FILING DATE: 2000-04-07
; PRIORITY FILING DATE: 09/170,496
; PRIORITY FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 562
; LENGTH: 1782
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-562

Query Match 72.7%; Score 959.6; DB 4; Length 1782;
Best Local Similarity 86.8%; Pred. No. 1.9e-254;
Matches 1081; Conservative 0; Mismatches 159; Indels 6; Gaps 2;

Qy 69 TGGCTGGAGGTATTTGACCGCTAGGCATGATFCTACACCGTGGGATACCTCAATGTCTCT 128
Db 537 TGAACGGAGGTGTTTGACCGCTGGCATGATTTACCGCTGGGCTACTCCGTGTCCCT 596
Qy 129 CGCTCCCTCAAGTGGCTGTGCTCATCTGGCTATTTAGCGGCTGCACTGCAAGCG 188
Db 597 GCGTCCCTCACCGTGTGCTCATCTGGCTACTTTAGCGGCTGCACTGCAAGCG 656
Qy 189 CAACATACCCACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 248
Db 657 CAACATACCCACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716
Qy 249 GAAGGACGCTGTGCTCTACTCTGGCTTACGCTGGATGAGGCGGCGCTCAGAGGA 308
Db 717 CAAGGACGCTGTGCTCTACTCTGGCGCCAGCTTGTATGAGGCTGAGCGCTCACCAGGA 776
Qy 309 AGAGTGGACATCATCGCGAGGTGCCACTCGCGCGGCGCTGCGCGCGCTAGGCTACGC 368
Db 777 GAGCTGCGCGCATCGCGAGGCGCGCGCGCGCTGCGCGCGCTGCGCGCGCTACGC 836
Qy 369 TGCTGCGCGCTGCGCTGAGCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 428
Db 837 GGGCTGAGGGTGGCTGTGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 896
Qy 429 CTTGTGGAGGGCTGTACTTGCACAGCCTCACTTCTCATGGCTTTTCTCAGAGAAGAA 488
Db 897 TCTGTGGAGGGCTGTACTTGCACAGCCTCACTTCTCATGGCTTTTCTTCTCAGAGAAGAA 956
Qy 489 GTACTGTGGGGCTTACCATCTTGTGGTGGGTCTACCGGCTGCTCTGCTGGCTGTGTG 548
Db 957 GTACTGTGGGGCTTACCATCTTGTGGTGGGTCTGCGCGCTGCTCTGCTGGCTGTGTG 1016
Qy 549 GGTGGTGTGAGAGCAACTTGGCCAACTTGGGTGCTGGGATCTGAGCTCCGGGACAA 608
Db 1017 GGTGAGTGTGAGAGCTACCTGCGCAACACCGGGTGTGAGCTCCGGGACAA 1076
Qy 609 GAAGTGGATCATCAGGTGCCATCTCTGGCATCTGTTGTGCTCAACTTCACTCTTTTAT 668
Db 1077 AAAGTGGATCATCAGGTGCCATCTCTGGCTCCTTCTGCTCAACTTCTCTCTCTCTCT 1136
Qy 669 CAACATCATCGGGTGTGCGCACTAAGCTTGGGAGACCAATGCGGCGGCTGTGACAC 728
Db 1137 CAATATGCTCCGGTGTGCTGCCACCAAGCTTGGGAGACCAACGCGCGGCTGTGACAC 1196
Qy 729 CAGCAGCAGTACCGAAGCTGCTCAGGTCCAGTGTGGTGTGCTGCTGCTGCTGCTGCTGCT 788
Db 1197 ACGGAGCAGTACCGAAGCTGCTCAATCCCGCTGGTGTGCTCATGCCCTCTTTGGCGT 1256
Qy 789 GCACTACCGCTCTTCAAGCTTGGCGTCAACCGAGGTCTCAGGAGCATTTGTGGCAGAT 848
Db 1257 CCACATCATTTCTTCTATGGCCACACCATACCGAGGTCTCAGGAGCGCTCTGGCAAGT 1316
Qy 849 CAGATGCATTATGAGTGTCTTCACTCTTCCAGGGATTTTGTGTCCTCATATATA 908
Db 1317 CCAGATGCATATGAGTGTCTTCACTCTTCCAGGGATTTTGTGTCCTCATATATA 1376
Qy 909 CTGTTTCTGCAATGGTGTGAGGTGAGGAGTCAAGCTGAGATCAAGAAATCTTGGAGCGCTGGAC 968
Db 1377 CTGTTTCTGCAATGGGAGGTGAGGAGTCAAGCTGAGATCAAGAAATCTTGGAGCGCTGGAC 1436
Qy 969 GCGCTGGAGCTTCAAGCGCAAGAGCAAGAGTGGAGGTAGCAGCTACAGCTATGCGCCCAAT 1028
Db 969 GCGCTGGAGCTTCAAGCGCAAGAGCAAGAGTGGAGGTAGCAGCTACAGCTATGCGCCCAAT 1028

Db 1437 GGCAGTGGACTTCAAGCGAAGGACGACGCGGGAGGACGAGCTATAGTACGGCCCAT 1496
Qy 1029 GGTGTCTCACAGAGTGTGACCAATGTGGGCCCCCGTGCAGAGTACAGCTCCCCCTCAG 1088
Db 1497 GGTGTCCACACAAAGTGTGACCAATGTGGGCCCCCGTGCAGAGTACAGCTCCCCCTCAG 1556
Qy 1089 CCCCCG---CTGGCTCTGCGCACTACCAATGGGCACTCCAGCTGCTGGCCATGCCAA 1145
Db 1557 CCCCCGCTTACTGCCCACTGCGCACCAACAGCGCCACCCTCAGCTGCTGGCCATGCCAA 1616
Qy 1146 GCCAGGGCTCCAGCACTGAGAC---TGAAACCTTACCAGTCACTATGGGGTTCCCAA 1202
Db 1617 GCCAGGACCCAGCCCTGGAGACCTCGAGACCACACACCTGCCATGGCTGTCCCAA 1676
Qy 1203 GGACATGGATTCTTAACGGCTCTGCTCAGGCTCGATGAGGAGGCTCCGGGTCTGC 1262
Db 1677 GGACATGGTTCTTCAACGGCTCTGCTCAGGCTCGACGAGGAGGCTCTGGGCTTGA 1736
Qy 1263 GCGGCGGCTCCATGTTGTCAGGAAGGATGGAAACAGTCACTGTA 1308
Db 1737 GCGGCCACTGCCCTGCTACAGGAAGTGGGAGACGTCATGTGA 1782

RESULT 7

US-07-864-475A-2
; Sequence 2, Application US/07864475A
; Patent No. 5494806
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, John T. [Jr.]
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
; TITLE OF INVENTION: AND DNA ENCODING SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864,475A
; FILING DATE: 04-06-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/681,702
; FILING DATE: 05-04-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/071002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1863
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-07-864-475A-2

Query Match

52.4%; Score 691.6; DB 1; Length 1863;

Best Local Similarity 74.2%; Pred. No. 1.7e-180;
Matches 925; Conservative 0; Mismatches 294; Indels 27; Gaps 3;
Qy 73 CTGAGAGTATTGTACCGCCTAGGCATGATCTACACCGTGGGATATCTCATCTCTCGCC 132
Db 629 CGGGAAGTCTTGTATCGCTCGGAATGATCTACACTGTGGGTACTCATCTCTCTGGGC 688
Qy 133 TCCCTCACTGGTGTGTGCTCATCTCGGCTATTTTAGGGGGTGCATGTGACGCGCAAC 192
Db 689 TCCCTCACTGGTGTGTGCTCATCTCGGCTATTTTAGGGGGTGCATGTGACGCGCAAC 748
Qy 193 TACATCCACATGACATGTTCTGCTGCTTTATGTGCGCGCGGAGCATCTTCGTGAAG 252
Db 749 TACATTCACATGACATCTCTTCTGCTGCTTTATGTCTCGGGCTGTGAAGCATCTTCATCAAG 808
Qy 253 GACCGCTGTGCTCTACTCTGCGCTTCAACGCTGAGTGGGCGGAGCGCTTACAGAGGAAGAG 312
Db 809 GATGCTGTGCTCTACTCTGCGGGTTCACAGATGAATCGAGCGCATCACCGAGGAGAG 868
Qy 313 TTGCACATCATCGCGCAGGTGCCACCTCCGCGGCGCTGCGCGCTGAGGTACGCTGGC 372
Db 869 CTGAGGGCTTTCACAGAG-----CCTCCCCCTGCTGACAAAGGGGGTTCGTGGGC 919
Qy 373 TGCGCGTGGGGTGAGCTTCTTCTCTACTCTTCTGCTGCTACCACTACTACTGATCCTG 432
Db 920 TGCAGAGTGGCGGTAAACCGCTTCTCTTACTTCTGACCACTACTACTGATCCTG 979
Qy 433 GTGAGGGGCTGTACTTTCACAGCCTCATCTTCATGGCTTTTCTCAGAGGAAGAATAC 492
Db 980 GTGGAAGGCTCTACTTTCACAGCCTCATCTTCATGGCTTTTCTCAGAGGAAGAATAC 1039
Qy 493 CTGTGGGGCTTTCACATCTTTTGGCTGGGGTTCACCGCTGCTTCGTGGGTGTGTGGTC 552
Db 1040 CTCTGGGGTTCACATATTATTTGGCTGGGGCTCCTCCGCTGCTTGTGCTGCTGGGTG 1099
Qy 553 GGTGTGAGAGCACTTGGCGCACTGGGTGCTGGGATCTGAGCTCGGGGCAAGAG 612
Db 1100 ACCGTGAGGGCTACACTGGCGCAACACTGAGTGTGGGACCTGAGTTCGGGGAATAAGAAA 1159
Qy 613 TGATCATTCAGGTGCGCCATCTTCTGCTCTGCTCACTCACTTCACTCTTTTATCAAC 672
Db 1160 TGGATCATACAGGTGCGCCATCTTGGGAGCTATTGTGGTGAATTTATCTTTTATCAAT 1219
Qy 673 ATCATCCGGTGTGCTGCTCACTAAGTTCGGGAGACCAATCGGGCCGGTGTGACACAGG 732
Db 1220 ATAATCAGAGTCTCTGGCTACTAACTCCGGGAGACCAATGCAGGGAGATGTGACACAGG 1279
Qy 733 CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGTCTGCTGGCTCTTTGGTGTGCAC 792
Db 1280 CAACAGTATAGAAAGCTGCTGAAGTCCACGCTAGTCTCATGCGCTATTTCGGGGTGCAC 1339
Qy 793 TACACCGTCTTCATGGGCTTTCGGTACACCGAGTCTCAGGACATTTGTGSCAGATCCAG 852
Db 1340 TACATGCTCTTCATGGCCACGCGGTACAGAGATATCAGGATTCCTTTGGCAAGTCCAA 1399
Qy 853 ATGCATTCAGATGCTCTTCAACTCTTCAGGAGATTTTGTGTCATATATCTGT 912
Db 1400 ATGCATTCAGATGCTCTTCAACTCTTCAGGAGATTTTGTGTCATATATATCTGT 1459
Qy 913 TTCTGCAATGCTGAGTGGCAGGACAGATTTAGGAGTTCATGGAGCCGCTGACACTGGCG 972
Db 1460 TTCTGCAATGAGAGGTACAGCAGAGATCAAGAAGTTCATGGAGCCGATGAGCCCTGGCC 1519
Qy 973 TTGGACTTCAAGCGCAAGCACGAAGTGGGAGTAGCAGCTACAGCTATGCGCCCAATGCTG 1032
Db 1520 TTGGACTTCAAGCGCAAGCGCCGAGGTGGCAGCAGTACCTACAGCTATGCGCCCAATGCTG 1579
Qy 1033 TCTCACACGAGTGTGACCAATGTGGGCCCCCGTGCAGGAGTCTCAGCTCCCTCAGCCCC 1092
Db 1580 TCACATACAGTGTTCACCAATGTGGGACCTCGAGGGGGGCTGGCCTTGTCCCTCAGCCCT 1639
Qy 1093 CGCTGCTCTCT-----GCCACTACCAATGGCCACTCCAGCTGCTCCGCTGCTGCGCATGCC 1143

Db 1640 CGACTAGCTCTGGGGCTGGAGCCAGTGCCAAATGGCCATCACCAAGTTGGCTTGGCTATGTG 1699
Qy 1144 AAGCAGGGGCTCAGCCACTGAGACTGAAACCCCTACCAGTCACTATGGGGTTCCCAAG 1203
Db 1700 AAGCATGGTTCCATTTCTGAGAACTCAATGGCTTTCACTCGGCCAGAGCCCTGGCACCAAA 1759
Qy 1204 GACGATGATTTCTTAACGGCTCTGCTCAGGCCCTGGATGAGGAGGCTCCGGGTCTGCG 1263
Db 1760 GATCAGGGGTATCTCAATGGCTCTGG-----ACTTATGAGCCAAATGGTTGGGGAA 1810
Qy 1264 CGCGCGCTCCATTTGTCAGGAGGATGGGAACACTGATGTGAC 1309
Db 1811 CAGCCCCCTCACTCTCTGGAGGAGAGAGACAGTCAATGTGAC 1856

RESULT 8

US-08-468-249A-2
; Sequence 2, Application US/08468249A
; Patent No. 5886148

GENERAL INFORMATION:

; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995

CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/864,475

; FILING DATE: 06-APR-1992

; APPLICATION DATA:

; APPLICATION NUMBER: US 07/681,702

; FILING DATE: 04-MAY-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Fraser, Janis K.

; REGISTRATION NUMBER: 34,819

; REFERENCE/DOCKET NUMBER: 00786/071003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1863 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 98...1853

US-08-468-249A-2

Query Match 52.4%; Score 691.6; DB 2; Length 1863;

Best Local Similarity 74.2%; Pred. No. 1.7e-180;

Matches 925; Conservative 0; Mismatches 294; Indels 27; Gaps 3;

Qy 73 CTGAGGATTTGACCGCTAGGATGATCTACACCGTGGGATCTCATGCTCTCTCGCC 132

Db 629 CGGGAAGTCTTTGATCGCCTCGGAATGATCTACACTGTGGGCTACTCCATCTCTCGGC 688

Qy 133 TCCCTCAGCGTGGCTGTGCTCATCTCGCCTATTTTAGGCGGCTGCACCTGCACCGCAAC 192

Db 689 TCCCTCACTGTGGCTGTGCTGATTCTTGGGGTTACTTTAGGAGGTTACATTCGACCCGAAAC 748
Qy 193 TACATCCAGTACATGACATGTTCTGTGTTATGCTGGCGCCGCGAGCATCTTCGTGAAG 252
Db 749 TACATTCACATGATCATCTCTTGTGTTGCTTTATGCTCCGGGCTGTAAGCATCTTCATCAAG 808
Qy 253 GACGCTGTGCTCTACTCTGCTTCAAGCTGGATGAGCGCGAGCGCTCTACAGAGGAAGAG 312
Db 809 GATGCTGTGCTCTACTCTGGGGTTTCCACAGATGAAATCGAGCGCATCACCGAGGAGAG 868
Qy 313 TCCACATCATTCGCGCAGGTGCGCACCTCGCGCCGCGCTGCCCGCTAGGCTACGCTGGC 372
Db 869 CTGAGGCGCTTACAGAG-----CCTCCCGCTGCTGACAAGCGGGTTTTGTGGGC 919
Qy 373 TGCCGCTGGCGGTGACCTTCTCTACTTCTGGCTACCACTACTACTGATCCTG 432
Db 920 TGCAGAGTGGCGGTAAACCGTCTTCTTACTTCTGACCAACCACTACTACTGATCCTG 979
Qy 433 GTGGAGGGGCTGTACTTGCACAGCCTCATCTTCATGCGCTTTTCTCAGAGAAGAGTAC 492
Db 980 GTGGAAGGCTCTACTTTCACAGCCTCATCTTCATGGCTTTTCTCTGAGAAAAGTAT 1039
Qy 493 CTGTGGGGCTTCAACCATCTTTGGCTGGGCTTACCGGCTGTCTTCGTGGCTGTGGGTC 552
Db 1040 CTCTGGGGTTTCAATTATTTGGCTGGGCTCTCCCTCGCGTGTTCGCTGTGGGTG 1099
Qy 553 GGTGTGAGAGCAACCTTTGGCCAACTCTGGGTGCTGGGATCTGAGCTCCGGGCAAGAAG 612
Db 1100 ACCGTGAGGGCTACACTGGCCAACTGAGTGTGGGACCTGAGTTTCGGGGAAATAAGAA 1159
Qy 613 TGGATCATCCAGGTGCCCATCTCTGGCATCTGTTGTGCTCAACTTCACTCTTTTATCAAC 672
Db 1160 TGGATCATACAGGTGCCCATCTCTGGCAGCTATTGTGTAACCTTTATCTTTTATCAAT 1219
Qy 673 ATCATCCGGTGTCTGCCACTAAGCTTCGGGAGACCAATCGCGGCGGTGTGACACAGG 732
Db 1220 ATAATCAGAGTCTCTGGCTACTAACTCCGGGAGACCAATGACGGAGATGTGACACAGG 1279
Qy 733 CAGCAGTACCGGAAGCTGTCTCAGGTCCAGTGTGGTGTCTCGTGGCTCTTTGGTGTGCAC 792
Db 1280 CAACAGTATAGAAAGCTGTCTGAAAGTCCAGCTAGTCTCATGCGCGTATTTCGGGGTGCAC 1339
Qy 793 TACACGCTCTTTCATGCGCTTGGCGTACACAGAGGTCTCAGGGACATTTGTGGAGATCCAG 852
Db 1340 TACATGCTCTTTCATGCGCAGCGGTACACAGAGTATCAGGGATTTCTTTGGCAAGTCCAA 1399
Qy 853 ATGCATTATGAGATGCTCTTCAACTCTTCCAGGGATTTTTCGTGCCATCATATACTGT 912
Db 1400 ATGCACTATGAAATGCTCTTCAATTCAATCCAGGGATTTTTCGTGGCATTTATATACTGT 1459
Qy 913 TTTCTGATGCTGAGGTGAGGCGAGAGATTAGGAAGTCTAGGAGCCGCTGGACACTGGCG 972
Db 1460 TTCTGCAATGGAGAGGTACAAAGAGATCAAGAAGTCTAGGAGCCGATGGAGCCCTGGCC 1519
Qy 973 TTGAGCTTCAAGCGCAAAAGCACCAAGTGGGAGTAGCAGCTACAGCTATATGGCCCAATGGTG 1032
Db 1520 TTGAGCTTCAAGCGGAAGGCGCGGAGTGGCAGCAGTACCTACAGCTATATGGCCCATGGTG 1579
Qy 1033 TCTCACAAGAGTGTGACCAATGTGGGCGCCCGGTGCGAGGACTACGCTCTCCCTTCAGCCCC 1092
Db 1580 TCACATACAGTGTCAACCAATGTGGGACCTCGAGGGGGGCTGGCCTTGTCCCTCAGCCCT 1639
Qy 1093 CGCTGCTCTCT-----GCCACTCAATGGCCATCTCCAGCTGCTGGCCATGCC 1143
Db 1640 CGACTAGTCTCTGGGCTGGAGCCAGTGGCAATGGCCATCCAGTTGCTGGCTATGTG 1699
Qy 1144 AAGCAGGGGCTCCAGCCACTGAGACTGAAACCCCTACCACTACTATGGCGGTTTCCCAAG 1203
Db 1700 AAGCATGGTTCCATTTCTGAGAACTCATTTGCCCTTCATCTGGCCGAGAGCTTGGCACCAAA 1759
Qy 1204 GACATGATGATTTCTTAACCGCTCTCTGCTCAGGCTGTGATGAGAGGCTCTCGGGTCTGCG 1263

Db	1760	GATGACGGGTATCTCAATGGCTCTGG-----ACTTTATGAGCCAATGTTGGGGAA	181
Qy	1264	CGCGCCCTCCATTGTTGCAGGAAGGATGGGAAACAGTCATGTGAC	1309
Db	1811	CAGCCCCCTCCACTCCTTGGAGGAGAGAGACAGTCATGTGAC	1856
RESULT 9			
US-07-864-475A-1			
; Sequence 1, Application US/07864475A			
; Patent No. 5494806			
; GENERAL INFORMATION:			
; APPLICANT: Segre, Gino V.			
; APPLICANT: Kronenberg, Henry M.			
; APPLICANT: Abou-Samra, Abdul-Badi			
; APPLICANT: Juppner, Harald			
; APPLICANT: Potts, John T. (Jr.)			
; APPLICANT: Schipani, Ernestina			
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR			
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR			
; NUMBER OF SEQUENCES: 17			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Fish & Richardson			
; STREET: 225 Franklin Street			
; CITY: Boston			
; STATE: Massachusetts			
; COUNTRY: U.S.A.			
; ZIP: 02110-2804			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb			
; COMPUTER: IBM PS/2 Model 502 or 55SX			
; OPERATING SYSTEM: MS-DOS (Version 5.0)			
; SOFTWARE: WordPerfect (Version 5.1)			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/07/864,475A			
; FILING DATE: 04-06-1992			
; CLASSIFICATION: 435			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 07/681,702			
; FILING DATE: 05-04-1991			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Paul T. Clark			
; REGISTRATION NUMBER: 30,162			
; REFERENCE/DOCKET NUMBER: 00786/071002			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (617) 542-5070			
; TELEFAX: (617) 542-8906			
; TELEX: 200154			
; INFORMATION FOR SEQ ID NO: 1:			
; SEQUENCE CHARACTERISTICS:			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: linear			
; US-07-864-475A-1			
Query Match 51.6%; Score 681.2; DB 1; Length 1862;			
Best Local Similarity 74.2%; Pred. No. 1.3e-177;			
Matches 925; Conservative 0; Mismatches 293; Indels 28; Gaps 4;			
Qy	73	CTGAGAGTATTGACCGCCTAGGCGATGATCTACACCGTGGGATCTCCATGTCTCTGCCC	132
Db	629	CGGGAAGCTTTTGATCGCCTCGGAATGATCTACACTGTGGGTACTCCATCTCTCTGGGC	688
Qy	133	TCCCTACGGTGGCTGTGCTCATCTCGGCCTATTTTAGCGGGCTGCACTGCGCGCAAC	192
Db	689	TCCCTCACTGTGGCTGTGCTGAITCTCGGGTTACTTTTAGGAGGTTTACATTGCAACCCGAAAC	748
Qy	193	TACATCCACATGCACATGTTCTTGTCGTTTATGTCGCGCGCGAGCATCTTTCGTGAAG	252
Db	749	TACATTCACATGCAATCTCTTCGTGTCTCTTATGTCCTCGGGCTGTAAAGCATCTTCATCAAG	808
Qy	253	GAGCTGTGCTCTACTCTGGCTTTCACGCTGGATGAGCGCGAGCGCCTTCACAGAGAGAGAG	312

US-08-468-249A-1	;	Sequence 1, Application US/08468249A	
;	;	Patent No. 5886148	
;	;	GENERAL INFORMATION:	
;	;	APPLICANT: Segre et al., Gino V.	
;	;	TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA	
;	;	TITLE OF INVENTION: ENCODING SAME	
;	;	NUMBER OF SEQUENCES: 21	
;	;	CORRESPONDENCE ADDRESS:	
;	;	ADDRESSEE: Fish & Richardson P.C.	
;	;	STREET: 225 Franklin Street	
;	;	CITY: Boston	
;	;	STATE: MA	
;	;	COUNTRY: USA	
;	;	ZIP: 02110-2804	
;	;	COMPUTER TYPE: Floppy disk	
;	;	COMPUTER: IBM PC compatible	
;	;	OPERATING SYSTEM: PC-DOS/MS-DOS	
;	;	SOFTWARE: Patent In Release #1.0, Version #1.30	
;	;	CURRENT APPLICATION DATA:	
;	;	APPLICATION NUMBER: US/08/468,249A	
;	;	FILING DATE: 06-JUN-1995	
;	;	CLASSIFICATION: 530	
;	;	PRIOR APPLICATION DATA:	
;	;	APPLICATION NUMBER: US 07/864,475	
;	;	FILING DATE: 06-APR-1992	
;	;	PRIOR APPLICATION DATA:	
;	;	APPLICATION NUMBER: US 07/681,702	
;	;	FILING DATE: 04-MAY-1991	
;	;	ATTORNEY/AGENT INFORMATION:	
;	;	NAME: Fraser, Janis K.	
;	;	REGISTRATION NUMBER: 34,819	
;	;	REFERENCE/DOCKET NUMBER: 00786/071003	
;	;	TELECOMMUNICATION INFORMATION:	
;	;	TELEPHONE: 617/542-5070	
;	;	TELEFAX: 617/542-8906	
;	;	INFORMATION FOR SEQ ID NO: 1:	
;	;	SEQUENCE CHARACTERISTICS:	
;	;	LENGTH: 1862 base pairs	
;	;	TYPE: nucleic acid	
;	;	STRANDEDNESS: single	
;	;	TOPOLOGY: linear	
;	;	FEATURE:	
;	;	NAME/KEY: CDS	
;	;	LOCATION: 98..1643	
;	;	US-08-468-249A-1	
Query Match	51.6%;	Score 681.2; DB 2; Length 1862;	
Best Local Similarity	74.2%;	Pred. No. 1.3e-177;	
Matches	925; Conservative	0; Mismatches 293; Indels 28; Gaps 4;	
QY	73	CTGAGGATTTGACCGCTAGGCATGATCTACACGGTGGGATCTCCATCTCTCTGCC	132
DB	629	CGGGAAGTCTTGATCGCTCGGAATGATCTACACTGTGGGCTACTCCATCTCTCTGGC	688
QY	133	TCCCTCAGCGTGCTGTGCTCATCTCGGCTATTTTAGCGGCTGCATCTGCACGGCAAC	192
DB	689	TCCCTCAGCTGGCTGTGCTGATCTGGGTACTTTAGAGGTTACATTCACCCGAAC	748
QY	193	TACATCCACATGCATGTTCTGTCTGTTTATGCTGCGCGCGCGAGCATCTTCGTGAAG	252
DB	749	TACATTCACATGCATCTCTTGTGTCTTTATGCTCGGGCTGTAAAGCATCTTCATCAAG	808
QY	253	GAGCGTGTGCTTACTCTGTGCTTACGCTGAGATGAGCGCGAGCGCTCACAGAGAAGAG	312
DB	809	GATGCTGTGCTTACTCTCGGGGGTTTCCACAGATGAATCGAGCGCATCACCGAGGAGAG	868
QY	313	TTGCACATCATCGCAGAGTGCACCTCCGCGCGCGCTGCCGCGTAGGCTACGCTGGC	372
DB	869	CTGAGGCGCTTACAGAG-----CTCCCTCTGCTGACAGGCGGGTTTGTGGGC	919
QY	373	TGCGCGGTGGCGGTGACCTTTCTCTCTACTTTCTGGGTACCAACTACTACTGATCTG	432


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Db      560  TTCTCTGGCTGTGGCTATCTCATCATTTGGTTACTTCAGACGATTCGATTCGACTAGGAA 619
Qy      192  CTACATCCACATGACATGTCCTGTGTGTATGCTGCGCGCGCGAGCATCTTCGTGAA 251
Db      620  CTATATCCACATGACATTAATTTGTGTCTTTTCATGCTGAGAGCTACAAGCATCTTTGTCAA 679
Qy      252  GGAGCGTGTGCTCTACTCTGGCTTCACGCTGGATGAGCGCGAGCGCTCACAGAGGAGA 311
Db      680  AGACAGAGTAGTCATGCTCACAATAGGAGTAAGAGCTGGAGTCCCTAATAATGACGGA 739
Qy      312  GTTCACATCATCCGCGAGGTGCCACCTCGCGCGCGCTGCCCGCTAGGCTACGCTGG 371
Db      740  TGACCCACAAAATTCATTTAGGCAAACTCTGTGGCAAAATC-----ACAAATATATCGG 793
Qy      372  CTGCGCGGTGGCGTGACCTTTCTCTACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
Db      794  GTGCAAGATTGCTGTGTGTGTATTTTATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
Qy      432  GGTGAGGGGTGTACTTGCACAGCCTCATCTTCATGCGCCTTTTCTCAGAGAGAGTA 491
Db      854  GGTGAGGGGTGTACTTGCACAGCCTCATCTTCATGCGCCTTTTCTCAGAGAGAGTA 913
Qy      492  CCTGTGGGGTTCACCATCTTTGGCTGGGTCTACCGGCTGTCTTCGTGGCTGTGTGGGT 551
Db      914  CCTGTGGGGTTCATCTTTAGAGCTGGGGTTTCCAGCAGCATTTGTTGCGCATGGGC 973
Qy      552  CGGTGTGAGAACACCTTTGGCAACACATGGGTGTGGATCTGAGCTCGCGGCAAGAA 611
Db      974  TGTGGCACAGCAACTCTGGCTGATGCGAGGTCTGGGAACTTAGTGTGGAGATCCAA 1033
Qy      612  GTGGATCATCCAGGTGCCATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
Db      1034  GTGGATTTATCAAGACCCGATCTTAGCAGCTATTTGGGCTGAAATTTTATCTGTCTTGAA 1093
Qy      672  CATCATCCGGGTCTTGGCCAACTTAAGCTTGGGAGACCAATGCGGGCGGTGTGACACCAAG 731
Db      1094  TAGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGAGTTGGGCAAGCAAG 1153
Qy      732  GCAGCAGTACCGAAGCTGCTCAGGTCCACGTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
Db      1154  GAAGCAATACAGGAAACTGGCCAAATCGACACTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1213
Qy      792  CTACACGCTTTCATGCGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851
Db      1214  TTACATCGTGTTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1270
Qy      852  GATGCATATGAGATGCTCTTCAACTCTTCCAGGATTTTGTGTCATCATATATCTG 911
Db      1271  CATGCATGTGAGCTCTTCTTCACTCTTCAAGGTTTCTTGTGTCTATCATCTACTG 1330
Qy      912  TTTCTGCAATGGTGTGAGGTGAGGAGAGTATAGGAGTGTGAGGCGGTGAGACATGGC 971
Db      1331  CTACTGCAATGGAGAGGTTTCAAGCAGAGGTGAAGAGATGTGGAGTGTGGAGTGTGGAGTGTGCTC 1390
Qy      972  GTTGGATCTCAAGCGCAAGCAAGCAAGTGGAGTAGCAGCTACAGCT 1018
Db      1391  CGTGGACTGGAAGAGGACACCGCCATGTGGAGCGCGCAGATGCGGCT 1437
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RESULT 13

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US-09-236-468A-1
; Sequence 1, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2003
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)..(1715)
US-09-236-468A-1
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Query Match      29.3%; Score 387.4; DB 3; Length 2003;
Best Local Similarity 64.6%; Pred. No. 1.5e-96;
Matches 612; Conservative 0; Mismatches 326; Indels 9; Gaps 2;
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Qy      72  GCTGGAGGTATTTGACGGCTTAGGCATGATCTACCGTGGGATACCTCATGCTCTCTCGC 131
Db      500  GCAAGAATCTGTGAAACGGCTCTATGTAATGTATACCGTTGGCTACTCCATCTCTTTGG 559
Qy      132  CTCCTTCACGGTGGCTGTGCTCATCTCTGGCTATTTTAGCGGCTGCACACGCGCAA 191
Db      560  TTCCTTGGCTGTGGCTATTTCTCATCATTTGGTTACTTCAGACGATTGCACTAGGAA 619
Qy      192  CTAATCCACAAACGACATGTTCTGTCTGCTTTATGCTGCGCGCGCAGACATCTTCGTGAA 251
Db      620  CTATATCCACATGCACTTAATTTGTGTCTTTTCATGCTGAGAGCTACAAGCATCTTTGTCAA 679
Qy      252  GGAGCGTGTGCTCTACTCTGGCTTCACGCTGGATGAGCGCGGCTCACAGAGGAGA 311
Db      680  AGACAGAGTAGTCCATGCTCACAATAGGAGTAAGAGAGCTGGAGTCCCTAATAATGACGGA 739
Qy      312  GTTGCACATCATCGCGCAGGTGCCACTCGCGCGCGCTGCGCGCTAGGCTACGCTGG 371
Db      740  TGACCCACAAAATTCATTTAGGCAAACTCTGTGGCAAAATC-----ACAAATATATCGG 793
Qy      372  CTGCGCGGTGGCGTGACCTTTCTCTACTCTTCTGGCTTACCAACTACTACTACTGATPCCT 431
Db      794  GTGCAAGATTGCTGTGTGTATTTTATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
Qy      432  GGTGAGGGGTGTACTTGCACAGCCTCATCTTCATGCGCCTTTTCTCAGAGAGAGTA 491
Db      854  GGTGAGAGGTCTCTACTGCAATATCTCATCTTTTGTGGCTTTCTTTTGGACACCAAAAT 913
Qy      492  CCTGTGGGGTTCACCATCTTTGGCTGGGTCTTACCGGCTGTCTTCGTGGCTGTGTGGGT 551
Db      914  CCTGTGGGGTTCATCTTTAGAGCTGGGGTTTCCAGCAGCATTTGTTGCGCATGGGC 973
Qy      552  CGGTGTGAGAACACCTTTGGCAACACATGGGTGTGGATCTGAGCTCGCGGCAAGAA 611
Db      974  TGTGGCACAGCAACTCTGGCTGATGCGAGGTCTGGGAACTTAGTGTGGAGATCCAA 1033
Qy      612  GTGGATCATCCAGGTGCCATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
Db      1034  GTGGATTTATCAAGACCCGATCTTAGCAGCTATTTGGGCTGAAATTTTATCTGTCTTGAA 1093
Qy      672  CATCATCCGGGTCTTGGCCAACTTAAGCTTGGGAGACCAATGCGGGCGGTGTGACACCAAG 731
Db      1094  TAGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGAGTTGGGCAAGCAAG 1153
Qy      732  GCAGCAGTACCGAAGCTGCTCAGGTCCACGTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
Db      1154  GAAGCAATACAGGAAACTGGCCAAATCGACACTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1213
Qy      792  CTACACGCTTTCATGCGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851
Db      1214  TTACATCGTGTTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1270
Qy      852  GATGCATATGAGATGCTCTTCAACTCTTCCAGGATTTTGTGTCATCATATATCTG 911
Db      1271  CATGCATGTGAGCTCTTCTTCACTCTTCAAGGTTTCTTGTGTCTATCATCTACTG 1330
Qy      912  TTTCTGCAATGGTGTGAGGTGAGGAGAGTATAGGAGTGTGAGGCGGTGAGACATGGC 971
Db      1331  CTACTGCAATGGAGAGGTTTCAAGCAGAGGTGAAGAGATGTGGAGTGTGGAGTGTGGAGTGTGCTC 1390
Qy      972  GTTGGATCTCAAGCGCAAGCAAGCAAGTGGAGTAGCAGCTACAGCT 1018
Db      1391  CGTGGACTGGAAGAGGACACCGCCATGTGGAGCGCGCAGATGCGGCT 1437
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Qy

972 GTTGGACTTCAGCGCAAAACGACGAAGCTGGGAGTAGCAGCTACAGCT 1018
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

D_b

1391 CGTGGACTGGAAAAGAACAACCCGCATGTGGCAGCCGCCAGATCGGGCT 1437
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RESULT 14

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PCT-US95-07085-1
/ Sequence 1, Application PC/TUS9507085
/ GENERAL INFORMATION:
/ APPLICANT: Soppet, Daniel R
/ APPLICANT: Soppet, Daniel R
/ APPLICANT: Yi, Li
/ APPLICANT: Rosen, Craig A
/ APPLICANT: Ruben, Steven
/ APPLICANT: Ruben, Steven
/ TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
/ TITLE OF INVENTION: HLTDG74
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
/ ADDRESSEE: Stewart & Olstein
/ STREET: 6 Becker Farm Road
/ CITY: Roseland
/ STATE: NJ
/ COUNTRY: USA
/ ZIP: 07068-1739
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/07085

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Query Match	29.3%	Score 387.4;	DB 5;	Length 2003;
Best Local Similarity	64.6%	Pred. No. 1.5e-96;		
Matches 612;	Conservative	0;	Mismatches 326;	Indels 99;
Gaps 2;				

		500	GGAAGAAATTCTGTGAAACGGCTCTATGTAANTGATACCGTTTGGGCTACTCCCATCTCTTTTG	555
Db				
		132	CTCCCTCACGGTGGCTGTGCTCATCCTCGGCCATATTTTAGCGCGCTGCACCTGCACGCGCAA	191
Qy				
		560	TTCCTTGGCTGTGGCTATTCTCATCATTTGGTTACTTCAGACGATTGCAATTCACCTAGGAA	619
Db				
		192	CTACATCCACATGCACATGTTCTCTGTCTTATGCTGGCGCGCGGANGANTCTTGGTGA	251
Qy				
		620	CTATATCCACATGCACCTATTTTGTGCTTTTCATGCTGAGAGCTACAAGCANCTTTGTCAA	679
Db				
		252	GGACGCTGTGCTCTACTCTGGCTTTCACGCTGGATGAGGCCCGAGCGCTCCACAGAGSAGA	311
Qy				
		680	AGACAGAGTAGTCATGCTCTCATATAGGAGTAAAGAGCTGGAATCCCTAATATGACAGA	739
Db				

RESULT 15

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RES001 15
US-09-449-632-3
; Sequence 3, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2152
; TYPE: DNA
; ORGANISM: zebrafish
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (394)..(2019)
; NAME/KEY: misc feature
; LOCATION: (2125)..(2125)

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OTHER INFORMATION: n is any nucleotide of a,t,g or c
US-09-449-632-3

Query Match 29.3%; Score 387.4; DB 4; Length 2152;
Best Local Similarity 65.4%; Pred. No. 1.5e-96;
Matches 608; Conservative 0; Mismatches 276; Indels 45; Gaps 1;

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Qy 68 ATGGCGCTGGAGGATTTTACCGGCTAGGCATGATCTACACGGTGGGATATCCATGTCTC 127
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 791 ATCAGGAGGAAGTGTGGCGGCTTTACCTCATGTACCTATTTGGATATCTCCATATCAC 850
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 128 TCGCCTCCCTCACGGTGGCTGTCTCATCTGGGCTATTTTAGCGGCTGCACCTGCACGC 187
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 851 TGGCAGGCTTACTGGTGGGCTCTATCTCTTCTATTTCAACGCTCTCCACTGCACCTC 910
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 188 GCAACTACATCCACATGATTTCTGTGGTATATGCTGGCGCGCGAGCATCTTCG 247
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 911 GTAACTACATCCACATCCACCTCTTACCTCGTTTATATGTCGAGCAATCAGTATTTTG 970
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 248 TGAAGGAGGCTGTCTCTACTTGTGCTTACCGCTGATGAGGCGGAGGCTCACAGAGG 307
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 971 TGAAGAGCGCGGTTCTTTACGCGCTCAGAAATGATGGAGAACTAGAAAGATGGGCGAGTGG 1030
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 308 AAGAGTTGCACATCATCGCGAGGTGCCACCTCGCGCGCGCTGCCGCGTAGGCTACG 367
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1031 AACAAAGACCAT-----GG 1045
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 368 CTGGCTCGCGGCTGGCGGTGACCTTCTCTCTACTTCTGGTACCAACTACTACTGGA 427
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1046 TGGGCTGCAAGGCTGTGTGACCTCTTCTCTGTATCTGTGGGACCAATCATTTATTGGA 1105
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 428 TCCTGGTGGAGGCGCTGTACTTGCACAGCCTCATCTTCATGGCCCTTTTCTCAGAGAAGA 487
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1106 TCCTGGTGGAGGCTTGTACTTGCATAGTCTGATCTTTCATGGCCCTCTCTGTCTGATAAGA 1165
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 488 AGTACTGTGGGCTTCCACATCTTGGCTGGGCTTACCGGCTGTCTTGGTGGCTGTGT 547
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1166 ACTGCTGTGGGCTTTGACAAATCATAGCTGGGGGATCCAGCAGTGTGTGTCTATAT 1225
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 548 GGGTCGGTGTCCAGAGCAACCTTGGCCAACTGGGTGCTGGGATCTGAGCTCCGGGCACA 607
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1226 GGGTCAGTGGCCAGGCTGTCTCTGGCAGACACAGTGTCTGGGATATCAGTGCAGGCAATT 1285
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 608 AGAAGTGGATCATCCAGTGGCCATCTCTGGCATCTGTGTGCTCAACTTCATCTTTTAA 667
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1286 TGAATGGATTTATCAAGTACCAATCTCGCAGCCATTTGTGTAAACTTCTCTCTCTCC 1345
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Qy 1346 TCAATATCATCAGGTTTTTGGCTCTAAGTTGTGGGAAACAAACACGGGAAACTGGACC 1405
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 728 CCAGGACAGTACCGGAAGCTGTCAAGTCCAGTGGTGGTGTCTCGTCCGCTCTTTGGTG 787
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1406 CTAGACAGCAGTACAGGAAGCTGTGAAGTCAACAATGGTGTCTGATGCCACTGTTGGAG 1465
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 788 TGCACACACCGCTTTCATGGCCCTTGGCTACACCGAGGCTCAGGACATTGTGGCAGA 847
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Qy 848 TCCAGATGCATTTATGAGATGCTTTCAACTCTTCCAGGGATTTTTTGTGGCCATCATAT 907
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Qy 1526 TTTCTGATGATATGAGATGCTCTTCAATCTTTCACAGGGTTCTTTGTGGCGTTTATTT 1585
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Qy 968 TGGGCTTGGACTTCAAGCGCAAGCAGA 996
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Qy 1646 TTGCGTTAGACCTGAAGCAGAAAGGCTGA 1674
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: July 4, 2005, 02:53:05

Job time : 260 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 4, 2005, 01:28:13 ; Search time 2710 Seconds
(without alignments)
3055.086 Million cell updates/sec

Title: US-09-869-565-1,
Perfect score: 1320
Sequence: 1 atgggggcccgcggatgcg.....tcattgtactgggcaactagg 1320

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 6313374 seqs, 3136092125 residues

Total number of hits satisfying chosen parameters: 12626748

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1243.2	94.2	2051	16 US-10-267-730-3	Sequence 3, Appli
2	1241.6	94.1	2065	18 US-10-152-319A-1741	Sequence 1741, Ap
3	1229.6	93.2	1776	9 US-09-943-446-3	Sequence 3, Appli
4	1146.4	86.8	1776	9 US-09-943-446-4	Sequence 4, Appli
5	1146.4	86.8	1776	9 US-09-943-446-5	Sequence 5, Appli
6	966.8	73.2	1948	15 US-10-225-567A-228	Sequence 228, App
7	966.8	73.2	1948	17 US-10-305-720-1253	Sequence 1253, Ap

8	966.8	73.2	1948	21	US-10-956-157-395	Sequence 395, App
9	966.8	73.2	2282	20	US-10-723-860-5567	Sequence 5567, Ap
10	965.2	73.1	2010	16	US-10-267-730-4	Sequence 4, Appli
11	965.2	73.1	2171	20	US-10-723-860-1005	Sequence 1005, Ap
12	959.6	72.7	1782	20	US-09-826-509-562	Sequence 562, App
13	959.6	72.7	1782	21	US-10-925-095-562	Sequence 562, App
14	958.2	72.6	1779	21	US-10-505-486-14	Sequence 14, Appli
15	902.2	68.3	2177	9	US-09-943-446-1	Sequence 1, Appli
16	899	67.5	1788	9	US-10-062-674-1564	Sequence 1564, Ap
17	758.4	57.5	2192	17	US-10-267-730-2	Sequence 2, Appli
18	691.6	52.4	1863	16	US-10-267-730-1	Sequence 1, Appli
19	681.2	51.6	1862	16	US-10-332-853-229	Sequence 229, App
20	610.8	46.3	1609	16	US-10-372-095-1	Sequence 1, Appli
21	554.6	42.0	1609	18	US-10-332-859-9	Sequence 9, Appli
22	462.4	35.0	637	18	US-10-295-027-523	Sequence 523, App
23	387.4	29.3	1896	17	US-09-996-569-1	Sequence 1, Appli
24	387.4	29.3	2003	9	US-10-921-218-1	Sequence 1, Appli
25	387.4	29.3	2003	21	US-10-372-095-3	Sequence 3, Appli
26	387.4	29.3	2152	16	US-10-225-567A-226	Sequence 226, App
27	387.4	29.3	2641	15	US-10-295-027-525	Sequence 525, App
28	387.4	29.3	2641	17	US-10-295-027-850	Sequence 850, App
29	387.4	29.3	2641	17	US-10-305-720-1463	Sequence 1463, Ap
30	387.4	29.3	2641	19	US-10-283-975A-70	Sequence 70, Appli
31	387.4	29.3	2641	20	US-10-723-860-2138	Sequence 2138, Ap
32	387.4	29.3	3071	20	US-10-723-860-6394	Sequence 6394, Ap
33	387.4	29.3	3071	20	US-09-826-509-564	Sequence 564, App
34	385.8	29.2	1653	10	US-10-925-095-564	Sequence 564, App
35	385.8	29.2	1653	21	US-10-956-157-5630	Sequence 5630, Ap
36	331.6	25.1	600	21	US-10-062-674-392	Sequence 392, App
37	328.6	24.9	343	17	US-10-017-161-709	Sequence 709, App
38	265	20.1	21704	15	US-10-292-798-621	Sequence 621, App
39	265	20.1	21704	17	US-09-968-007A-104	Sequence 104, App
C 40	241.8	18.3	509	11	US-09-968-007A-336	Sequence 336, App
C 41	241.8	18.3	509	11	US-09-968-007A-724	Sequence 724, App
C 42	241.8	18.3	509	21	US-10-843-641A-5574	Sequence 5574, Ap
C 43	241.8	18.3	509	21	US-10-843-641A-6806	Sequence 6806, Ap
C 44	241.8	18.3	509	21	US-10-843-641A-7194	Sequence 7194, Ap
C 45	241.8	18.3	509	21		

ALIGNMENTS

RESULT 1

US-10-267-730-3
; Sequence 3, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2051
; TYPE: DNA
; ORGANISM: Rattus rattus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)...(1845)
US-10-267-730-3

Query Match 94.2%; Score 1243.2; DB 16; Length 2051;
Best Local Similarity 99.8%; Pred. No. 0;

Qy 1213 TTCCTTAACGGCTCTCTGCTCAGGCTTGATGAGGAGGCTTCGGGTCTGCGCGCGCGCT 1272
Db 1681 TTCCTTAATGGCTCTCTGCTCGGGTCTGATGAGGAGGCTCTGGGTCTGCGCGCGCACT 1740
Qy 1273 CCATTGTTGACGAGGATGGAAACAGTCATGTGA 1308
Db 1741 CCATTGTTGACGAGGAAATGGAAACAGTCATGTGA 1776

RESULT 5
US-09-943-446-5
; Sequence 5, Application US/09943446
; Patent No. US2002014677A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-943-446-5

Query Match 86.8%; Score 1146.4; DB 9; Length 1776;
Best Local Similarity 95.5%; Pred. No. 0;
Matches 1180; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 73 CTGAGGTATTGACCGCTAGGCGATGATCTACACCGTGGGATCTCCATGCTCTCGCC 132
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Qy 133 TCCTCAGGTGCTGTGCTCATCTGCGCTATTTTGGCGGTGCACTGCAACGCGCAAC 192
Db 601 TCCTCAGGTGCTGTGCTCATCTGCGCTATTTTGGCGGTGCACTGCAACGCGCAAC 660
Qy 193 TACATCCACATGCACATGTTCTCTGCTTTATGCTGCGCGCGGAGCATCTTGTGAAG 252
Db 661 TACATCCACATGCACATGTTCTCTGCTTTATGCTGCGCGCGGAGCATCTTGTGAAG 720
Qy 253 GACGCTGTGCTTACTCTGCTTTCACGCTGATGAGCGCGGCTTACAGAGGAAGAG 312
Db 721 GACGCTGTGCTTACTCTGCTTTCACGCTGATGAGCGCGGCTTACAGAGGAAGAG 780
Qy 313 TTGCATCATATCGCGAGGTGCGACCTCCGCGCGCGCTGCGCGGTGAGCTACGCTGGC 372
Db 781 TTGCATCATATCGCGAGGTGCGCGCTCCGCGCGCGCTGCGCGGTGAGCTACGCTGGC 840
Qy 373 TGCGCGTGGCGGTGACCTTCTCTCTACTTCTGCTGCTACCACTACTACTGATCCTG 432
Db 841 TGCGCGTGGCGGTGACCTTCTCTCTACTTCTGCTGCTACCACTACTACTGATCCTG 900
Qy 433 GTGAGGGGTGTACTTTGACAGGCTCATCTTATGCGCTTTTCTCAGAGGAAGATAC 492
Db 901 GTGAGGGGTGTACTTTACAGGCTCATCTTATGCGCTTTTCTCAGAGGAAGATAT 960
Qy 493 CTGTGGGGCTTACCATCTTTGGTGGGGTCTACCGGCTGTCTTCTGCGGTGTGGGTC 552
Db 961 CTGTGGGGCTTACCATCTTTGGTGGGGTCTGCGGCTGTCTTCTGCGGTGTGGGTC 1020
Qy 553 GGTGTACAGCAACCTTGGCCAAACATCTGGGTGCTGGGATCTGAGCTCGGGGCAACGAAG 612
Db 1021 GGTGTACAGCAACCTTGGCCAAACATCTGGGTGCTGGGATCTGAGCTCGGGGCAACGAAG 1080

Qy 613 TGGATCATCCAGGTGCCATCTCTGCGCATCTGTGTCTCAACTTTCATCTCTTTTATCAAC 672
Db 1081 TGGATCATCCAGGTGCCATCTCTGCGCATCTGTGTGTCTCAACTTTCATCTCTTTTATCAAC 1140
Qy 673 ATCATCCGGGTGCTTGGCACTTAAGCTTCGGGAGACCAATCGGGCGGTGTGACACGAG 732
Db 1141 ATCATCCGGGTGCTTGGCACTTAAGCTTCGGGAGACCAATCGGGCGGTGTGACACGAG 1200
Qy 733 CAGCAGTACCGGAAGCTGCTCAGGTCCACCTTGGTGTCTGCTGCGGCTCTTTGGGTGTGAC 792
Db 1201 CAGCAGTACCGGAAGCTGCTCAGGTCCACCTTGGTGTCTTGTGCACTCTTCGGGTGTGAC 1260
Qy 793 TACACGCTCTTCATGGCTTGGCGTACACCGAGGTCTCAGGAGACATTTGTGCGAGATCCAG 852
Db 1261 TACACGCTCTTCATGGCTTGGCGTACACCGAGGTCTCAGGAGACATTTGTGCGAGATCCAG 1320
Qy 853 ATGCATATGAGATGCTCTTCAACTCTCTCCAGGATTTTGTGCGCATCATATCTGT 912
Db 1321 ATGCATATGAGATGCTCTTCAACTCTCTCCAGGATTTTGTGCGCATCATATCTGT 1380
Qy 913 TTCTGCAATGCTGAGGTGCGAGGAGATTTAGGAAGTCTTGGAGCGCTTGGACACTGGCA 972
Db 1381 TTCTGCAATGCTGAGGTGCGAGGAGATTTAGGAAGTCTTGGAGCGCTTGGACACTGGCA 1440
Qy 973 TTGGACTTCAAGCGCAAGCAACGAGGTGGAGTAGCAGCTACAGCTATGCCCCAATGGTG 1032
Db 1441 TTGGACTTCAAGCGTAAAGCAACGAGGTGGAGTAGCAGCTACAGCTATGCCCCAATGGGT 1500
Qy 1033 TCTCACAGAGTGTGACCAATGTGGGCGCGCTGCGAGGCTCAGGCTCTCCCTCAGGCCC 1092
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Qy 1093 CGCTGCTCTCTGCACTACCAATGCGCACTCCAGCTGCTGCGCATGCGCAAGCGAGGG 1152
Db 1561 CGCTGCTCTCTGCACTACCAATGCGCACTCCAGCTGCTGCGCATGCGCAAGCGAGGG 1620
Qy 1153 GCTCCAGGCACTGAGACTGAAACCTTACCAGTCACTATGCGGTTCCTCAAGGAGATGGA 1212
Db 1621 GCTCCAGGCACTGAGACTGAAACCTTACCAGTCACTATGAGAGTTCCTCAAGGAGAGGG 1680
Qy 1213 TTCTTAAAGGCTCTGCTCAGGCTGCGATGAGGAGGCTTCCGGGTCTGCGCGCGCGCT 1272
Db 1681 TTCTTAAAGGCTCTGCTCAGGCTTGGATGAGGAGGCTTCCGGGTCTGCGCGCGCACCT 1740
Qy 1273 CCATTGTTGACGAGGATGGGAAACAGTCATGTGA 1308
Db 1741 CCATTGTTGACGAGGATGGGAAACAGTCATGTGA 1776

RESULT 6

US-10-225-567A-228
; Sequence 228, Application US/10225567A
; Publication No. US2003011379A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-228

Query Match		73.2%;	Score 966.8;	DB 15;	Length 1948;		
Best Local Similarity		86.6%;	Pred. No. 3.4e-285;				
Matches 1090;		Conservative	0;	Mismatches 162;	Indels	6;	Gaps 2;
Qy	69	TGCGCTGGAGGTATTTGACCGCTTAGCATATCTACACCTGGGATACCTCAATGCTCT	128				
Db	565	TGAACGGGAGGTGTTGACCGCTGGCATGATTTACACCTGGGCTACTCCGTGTCCT	624				
Qy	129	CGCTCCCTCACGCTGCTGCTCATCTGGCCATTTTAGGGGCTGCACTGCAGCG	188				
Db	625	GGCTCCCTCACGCTGCTGCTCATCTGGCCATTTTAGGGGCTGCACTGCAGCG	684				
Qy	189	CAACTACATCACATGACATGTTCTGCTGTTATGCTGCGCCGCGGAGCATCTTCGT	248				
Db	685	CAACTACATCACATGACATGTTCTGCTGTTATGCTGCGCCGCGGAGCATCTTCGT	744				
Qy	249	GAAGGACGCTGTCTACTCTGGCTTTCAGCTGGATGAGGCGGAGCGCTTCAAGAGGA	308				
Db	745	CAAGGACGCTGTCTACTCTGGCGCACGCTTGATGAGGCTGAGGCGCTCACCGAGGA	804				
Qy	309	AGAGTTGCACATCATCGGAGGTGCCACCTCGCGCGCGCTGCGCGGTAGGCTACGC	368				
Db	805	GGAGCTCGCGCCATCGCGAGGTGCCACCTCGCGCGCGCTGCGCGGTAGGCTACGC	864				
Qy	369	TGGCTGCGCGGTGGCGGTGACCTTCTCTACTCTGCTGCTACCACTACTACTGGAT	428				
Db	865	GGCTGCGAGGTGGCTGACCTTCTCTACTCTGCTGCTACCACTACTACTGGAT	924				
Qy	429	CCTGGTGGAGGGCTGTACTTGCAACGCTCATCTTCATGCGCTTTCTCAGAGAAGAA	488				
Db	925	TCTGGTGGAGGGCTGTACTTGCAACGCTCATCTTCATGCGCTTTCTCAGAGAAGAA	984				
Qy	489	GTACTGTGGGGCTTACACATCTTGGCTGGGTCTACCGGCTCTTCGTGGCTGTG	548				
Db	985	GTACTGTGGGGCTTACACATCTTGGCTGGGTCTACCGGCTCTTCGTGGCTGTG	1044				
Qy	549	GGTGGGTGTCAGACCACTTGGCAACACTGGGTGCTGGATCTGAGCTCGGGACAA	608				
Db	1045	GGTGGGTGTCAGACCTTGGCAACACTGGGTGCTGGATCTGAGCTCGGGACAA	1104				
Qy	609	GAAGTGGATCATCAGGTGCCATCTTGGCATCTGTTGCTCAACTTCATCTTTTAT	668				
Db	1105	AAAGTGGATCATCAGGTGCCATCTTGGCATCTGTTGCTCAACTTCATCTTTTAT	1164				
Qy	669	CAACATCATCGGGTGTCTGCACTAGCTTCGGGACCACTAGCTGGGCGGTGTGACAC	728				
Db	1165	CAATATCTCGGGTGTCTGCACTAGCTTCGGGACCACTAGCTGGGCGGTGTGACAC	1224				
Qy	729	CAGGACGAGTACCGGAGCTGCTCAGTCCACGTTGGTGTCTGCTGGCTCTTTGGGT	788				
Db	1225	ACGGACGAGTACCGGAGCTGCTCAGTCCACGTTGGTGTCTGCTGGCTCTTTGGGT	1284				
Qy	789	GCACTACACCGTCTTCAATGCGCTTGGCCGTACACCGAGGTCTCAGGACATTTGGGAGAT	848				
Db	1285	CCACTACATTTCTTCAATGCGCTTGGCCGTACACCGAGGTCTCAGGACATTTGGGAGAT	1344				
Qy	849	CCAGATGATATGAGATGCTTCAACTCTTCCAGGATTTTTTTTGGGATCATATA	908				
Db	1345	CCAGATGATATGAGATGCTTCAACTCTTCCAGGATTTTTTTTGGGATCATATA	1404				
Qy	909	CTGTTCTGCAATGAGGTGAGGAGGAGGATTTAGGAGTCAAGGAGCGCTGGACACT	968				
Db	1405	CTGTTCTGCAATGAGGTGAGGAGGAGGATTTAGGAGTCAAGGAGCGCTGGACACT	1464				
Qy	969	GGCGTTGAGCTTCAAGCGCAAGACGAGGTGGAGTAGCAGCTACAGCTATGCGCCAAAT	1028				
Db	1465	GGCACTGAGCTTCAAGCGCAAGACGAGGTGGAGTAGCAGCTACAGCTATGCGCCAAAT	1524				
Qy	1029	GGTGTCTCACAGAGTGTACCAATGTGGGCCCCCGGTGAGGATCTAGGCTCCCGCTCAG	1088				
Db	1525	GGTGTCTCACAGAGTGTACCAATGTGGGCCCCCGGTGAGGATCTAGGCTCCCGCTCAG	1584				
Qy	1089	CCCCCGC---CTGGCTCTCGCCACTACCAATGGGCACTCCCAAGCTGCTGGCCATGCCAA	1145				

RESULT 7

US-10-305-720-1253
; Sequence 1253, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1253
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g190721
US-10-305-720-1253

Query Match 73.2%; Score 966.8; DB 17; Length 1948;
Best Local Similarity 86.6%; Pred. No. 3.4e-285;
Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2;

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Db	565	TGAACGGGAGGTGTTGACCGCTGGCATGATTTACACCGTGGGCTACTCCGTGTCCT	624				
Qy	129	CGCTCCCTCACGCTGCTGCTCATCTGGCCATTTTAGGGGCTGCACTGCAGCG	188				
Db	625	GGCTCCCTCACGCTGCTGCTCATCTGGCCATTTTAGGGGCTGCACTGCAGCG	684				
Qy	189	CAACTACATCCACATGCACATGTTCTGCTGCTTATGCTGCGCGCGGAGCATCTTCGT	248				
Db	685	CAACTACATCCACATGCACATGTTCTGCTGCTTATGCTGCGCGCGGAGCATCTTCGT	744				
Qy	249	GAAGGACGCTGTCTACTCTGGCTTTCAGCTGGATGAGGCGGAGCGCTCACAGAGGA	308				
Db	745	CAAGGACGCTGTCTACTCTGGCGCACGCTTGATGAGGCTGAGGCGCTCACCGAGGA	804				
Qy	309	AGAGTTGCACATCATCGGAGGTGCCACCTCGCGCGCGCTGCGCGGTAGGCTACGC	368				
Db	805	GGAGCTCGCGCCATCGCCAGGCGCCCGCGCGCTGCCACCGCGCTGCCGCTACGC	864				
Qy	369	TGGCTGCGCGGTGGCGGTGACCTTCTCTACTCTGCTTACTCTGCTTACTACTGGAT	428				
Db	865	GGCTGCGAGGTGGCTGACCTTCTCTACTCTGCTTACTCTGCTTACTACTGGAT	924				
Qy	429	CCTGGTGGAGGGCTGTACTTGCAACGCTCATCTTCATGCGCTTTTCTCAGAGAAGAA	488				
Db	925	TCTGGTGGAGGGCTGTACTTGCAACGCTCATCTTCATGCGCTTCTCTCAGAGAAGAA	984				
Qy	489	GTACTGTGGGGCTTACCAATCTTGGCTGGGTCTACCGGCTCTTCGTGGCTGTG	548				


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QY 1089 CCCCCG---CTGCTCTGCACTACCAATGGCCACTCCAGCTGCTGCTGCCATGCCAA 1145
Db 1585 CCCCCGCTTCTGCGCACTGCCACCAACAGCGCCACCTCAGCTGCTGCCATGCCAA 1644
QY 1146 GCCAGGGGCTCCAGCCCACTGAGAC---TGAAACCTTACCAGTCACTATGGCGGTCCCAA 1202
Db 1645 GCCAGGACCCAGCCCTGGAGACCTCGAGACACACCACTGCCATGCTGCCAA 1704
QY 1203 GGACGATGAGATTCCTTAACGGCTCTGCTCAGGCTCGATGAGAGGCTCCGGGTCTGC 1262
Db 1705 GGACGATGGGTTCCTCAACGGCTCTGCTCAGGCTCGAGAGGAGGCTCTGGGCTGA 1764
QY 1263 GCGGCCGCTCCATGTTGAGGAGGATGGAAACAGTCACTGATGGGCACTAGG 1320
Db 1765 GCGGCCACCTGCTCTACAGGAAGAGTGGGAGACAGTCACTGTGACAGGCGCTGG 1822

RESULT 9
US-10-723-860-5567
; Sequence 5567, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723.860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5567
; LENGTH: 2282
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2172)..(2279)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-5567

Query Match 73.2%; Score 966.8; DB 20; Length 2282;
Best Local Similarity 86.6%; Pred. No. 3.6e-285;
Matches 1090; Conservative 0; Mismatches 162; Indels 6; Gaps 2;

QY 69 TGGCTGGAGGTATTTGACCGCCTAGGCATGATCTACACCGTGGGATCTCCATGCTCT 128
Db 755 TGAACGGAGGTGTTTACCGCCTGGGCATGATTTACACCGTGGGCTACTCCGCTGCTCT 814
QY 129 CGCTCCCTCAGCGTGGCTGTGCTCATCTCGGCTATTTTAGCGGCTGCACTGCACGCG 188
Db 815 GGGCTCCCTCAGCTAGTGTGCTCATCTCGGCTACTTTAGGGGCTGCACTGCACGCG 874
QY 189 CAATCATCATCATGACATGTTCTGTGTGTTTATGCTGCGCGCCGAGCATCTTTCGT 248
Db 875 CAATCATCATCATGACATGTTCTGTGTGTTTATGCTGCGCGCCGCTGAGCATCTTTCGT 934
QY 249 GAGGAGCGCTGTGCTCTACTCTGCTTTCAGCTGGATGAGCGCGAGCGCTCAGAGGA 308
Db 935 CAAGGAGCGCTGTGCTCTACTCTGCGGCACGCTTGTATGAGGCTGAGCGCTCACCAGGA 994
QY 309 AGAGTTGCACATCATCGCGAGGTGCCACCTCCCGCGCGGCTGCGCGCTAGGCTACGC 368
Db 995 GGAGCTGGCGCCATCGCCAGGCGCCCGCGCGCTGCCACCGCGCTGCGGCTAGCG 1054
QY 369 TGGCTGCGCGGTGCGGTGAGCTTCTTCTCTACTTCTGCTTCTGCTTCTGCTTCTGCT 428
Db 1055 GGGCTGAGGCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 1114

; Sequence 4, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
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Db 935 CAAGGACGCTGTCTCTACTCTGCGGCCACGCTTGATGAGGCTGAGCGCTCAACCGAGGA 994
Qy 309 AGAGTTGCACATCATCCGCGAGGTGCCACCTCCGCGCGCGCTGCGCGCTAGGCTACGC 368
Db 995 GGAGCTCGCGCCATCCGAGGCGCCGCGCGCTGCCACCGCGCTGCGCGCTACGC 1054
Qy 369 TGGCTCGCGGTGGCGGTGACCTTCTTCCTACTCTCTGCTGCTACCAACTACTACTGGAT 428
Db 1055 GGGCTGAGGGTGGCTGTGACCTTCTTCCTTACTCTCTGGCCACCAACTACTACTGGAT 1114
Qy 429 CTTGGTGGAGGGGTGTACTTGACAGCCTCATCTTCATGGCCCTTTTTCTCAGAGAAGAA 488
Db 1115 TCTGGTGGAGGGGTGTACTTGACAGCCTCATCTTCATGGCCCTTCTTCTCAGAGAAGAA 1174
Qy 489 GTACTGTGGGGTTCACCAATCTTTGGCTGGGTCTACCGGCTGTCTTCGTGGCTGTGTG 548
Db 1175 GTACTGTGGGGTTCACAGTCTTCGGCTGGGGTCTGCCGCTGTCTTCGTGGCTGTGTG 1234
Qy 549 GGTGGGTGTGAGAACACCTTGGCCAACTTGGGTGCTGGGATCTGAGCTCCGGGCACAA 608
Db 1235 GGTGAGTGTGAGAGTACCTTGGCCAACTTGGGTGCTGGGATCTGAGCTCCGGGAACAA 1294
Qy 609 GAAGTGGATCATCCAGGTGCCATCTCTGGCATCTGTGTGCTCAACTTCACTCTTTTAT 668
Db 1295 AAAGTGGATCATCCAGGTGCCATCTCTGGCTCCATTTGTCTCAACTTCACTCTTTAT 1354
Qy 669 CAACATCATCCGGTGTCTTGGCATTAAGCTTGGGAGACCAATGCGGGCGGTGTGACAC 728
Db 1355 CAATATCTCGGGTGTCTGCCAACAAAGCTTGGGAGACCAACGCGCGCGGTGTGACAC 1414
Qy 729 CAGGACAGTACCGGAAGCTGTCTGAGTCCAGCTTGGTGTCTGTGCGGTCTTTTGTGT 788
Db 1415 ACGGACAGTACCGGAAGCTGTCTCAATCACTGTGTCTCATGCCCCCTCTTTGGCT 1474
Qy 789 GCACTACACCGCTTTCATGGCTTTGCCGTACACCGAGTCTCAGGGACATTTGGGCAGAT 848
Db 1475 CCACTACATTTCTTCATGGCCACACCATACCGAGTCTCAGGAGCGCTCTGGCAAGT 1534
Qy 849 CCAGATGCATTAAGATGTCTTCAACTCTCTCCAGGGAATTTTGTGGCATCATATA 908
Db 1535 CCAGATGCATTAAGATGTCTTCAACTCTCTCCAGGGAATTTTGTGGCATCATATA 1594
Qy 909 CTGTTTCTGCAA TGGTCAGGTGACGAGCAGAGTATPAGGAAGTCAAGGAGCGCTGGACCT 968
Db 1595 CTGTTTCTGCAA CGCGAGGTACAGCTGAGTACAGAAATCTTTGGAGCGCTGGACCT 1654
Qy 969 GGGCTTGGACTTCAAGCGCAAAGCACGAAGTGGAGTAGCAGCTACAGCTATGGCCCAAT 1028
Db 1655 GGCACTGGACTTCAAGCGAAAGGCACGACGCGGAGCAGAGCTATAGCTACGGCCCAT 1714
Qy 1029 GGTGTCTCACAGAGTGTACCAATGTGGGCCCCCGTGGAGGACTCAGGCTCCGCTCAG 1088
Db 1715 GGTGTCCACACAAAGTGTACCAATGTGGGCCCCCGTGGGACTCAGGCTCCGCTCAG 1774
Qy 1089 CCCCCGCG --CTGGCTCTGCACTACCAATGGGCACTCCAGCTGCTGGCCATGCAAA 1145
Db 1775 CCCCCGCTACTGCGCCACTGCAACCAACAGGCCACCTCAGCTGCTGGCCATGCAAA 1834
Qy 1146 GCCAGGGGCTCCAGCCACTGAGAC --TGAAACCTTACCAGTCACTATGGCGGTCCCAA 1202
Db 1835 GCCAGGGACCCAGCCCTGGAGACCCCTCGAGACCACACCACTGCGCATGCTGCCAA 1894
Qy 1203 GGACGATGGATTCCTTAACGGCTCTCTCAGGCTCGATGAGGAGCGCTCCGGGTCTGC 1262
Db 1895 GGACGATGGGTTCCTCAACGGCTCTCTCAGGCTTGGAGGAGGAGGCTCTGGGCTGA 1954
Qy 1263 GCGGCGGCTCCATTTGTCAGGAAGGATGGGAACAGTCACTGATGGGCACTAGG 1320
Db 1955 GCGGCCACCTGCTCTACAGGAAGATGGGAGACAGTCACTGATGACAGCGCTGGG 2012

RESULT 12

US-09-826-509-562

; Sequence 562, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 562
; LENGTH: 1782
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-826-509-562

Query Match 72.7%; Score 959.6; DB 10; Length 1782;

Best Local Similarity 86.8%; Pred. No. 5.2e-283;

Matches 1081; Conservative 0; Mismatches 159; Indels 6; Gaps 2;

Qy 69 TGGCTGGAGGTATTTGACCGCCTAGGCATGATCTACACGCTGGGATCTCATGTCTCT 128
Db 537 TGAACGGGAGGTCTTTGACCGCCTGGGCATGATTTACCGTGGGCTACTCGGTGCCCT 596
Qy 129 CGCTCCCTCACGGTGGCTGTCTCATCTGGCTATTTTGGCGGCTGCACTGCACGCG 188
Db 597 GGGTCCCTCACCGTAGTGTCTCATCTGGCTACTTTAGCGGCTGCACTGCACGCG 656
Qy 189 CAACTACATCCACATGACATGTTCTGTGCTTTATGCTGCGCGCGCGAGCATCTTCGT 248
Db 657 CAACTACATCCACATGACATGTTCTGTGCTTTATGCTGCGCGCGGTGAGCATCTTCGT 716
Qy 249 GAAGGACGCTGTCTCTACTCTGGCTTACGCTGGATGAGCGCGAGGCGCTCAGAGGA 308
Db 717 CAAGGACGCTGTCTCTACTCTGGCGCCACGCTTGTATGAGGCTGAGCGCTCACCAGGA 776
Qy 309 AGAGTTGCACATCATCGCGCAGGTGCCACCTCCGCGCGCGCTGCGCGCTAGGCTACGC 368
Db 777 GAGCTGCGGCCCATCGCCGAGCGGCCCGCGCGCTGCCACCGCGCTGCCGCTACGC 836
Qy 369 TGGCTGCGCGGTGGCGGTGACCTTCTTCCTCTACTTCTGGCTTACCAACTACTTGGAT 428
Db 837 GGGCTGCGAGGTGGCTGTGACCTTCTTCCTTACTTCTTGGCCACCAACTACTTGGAT 896
Qy 429 CTTGGTGGAGGGCTGTACTTGCACAGCCTCATCTTCATGGCCCTTTTCTCAGAGAAGAA 488
Db 897 TCTGGTGGAGGGCTGTACTCTGCACAGCCTCATCTTCATGGCCCTTCTTCTCAGAGAAGAA 956
Qy 489 GTACCTGTGGGGCTTCAACCATCTTTGGCTGGGTCTACCGGCTGTCTTCGTGGCTGTGTG 548
Db 957 GTACCTGTGGGGCTTCAACAGTCTTCGGCTGGGTCTGGCCGCTGTCTTCGTGGCTGTGTG 1016
Qy 549 GGTGGGTGTGAGAGCAACCTTGGCCAACTTGGGTGTGGGATCTGAGCTCCGGGCACAA 608
Db 1017 GGTGAGTGTGAGAGTACCTTGGCCAACTTGGGTGTGGGATCTTGGCTCCGGGAACAA 1076
Qy 609 GAAGTGGATCATCAGGTGCCATCTCTGGCATCTGTGTGCTCAACTTCACTCTTTTAT 668
Db 1077 AAAGTGGATCATCAGGTGCCATCTCTGGCTCCATTTGTGCTCAACTTCACTCTTCAT 1136
Qy 669 CAACATCATCCGGTGTCTTGGCACTAAGCTTGGGAGACCAATGCGGGCGGTGTGACAC 728
Db 1137 CAATATGTCGGGGTGTCTGCGCACCAAGCTGCGGAGACCAACGCGCGCGGTGTGACAC 1196
Qy 729 CAGGCAGCAGTACCGGAAGCTGTCTGAGTCCAGTGGTGTCTGTGCGGCTCTTTGTGTGT 788

QY 1203 GGAGATGGATTCTTAACGGCTCTCTCAGGCTGGATGAGGAGCCCTCCGGTCTGC 1262
DB 1677 GGACGATGGGTTCTTAACGGCTCTCTCAGGCTGGATGAGGAGCCCTCTGGGCTGA 1736
QY 1263 GCGGCCCGCTCCATTGTTGACGAGGATGGGAAACAGTGTATGTA 1308
DB 1737 GCGGCCACCTGCCCTGCTCAGGAGAGAGTGGGACAGTGTATGTA 1782

RESULT 14

US-10-505-486-14
; Sequence 14, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 14
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Human
US-10-505-486-14

Query Match 72.6%; Score 958.2; DB 21; Length 1779;

Best Local Similarity 86.8%; Pred. No. 1.4e-282;
Matches 1079; Conservative 0; Mismatches 158; Indels 6; Gaps 2;

QY 69 TGGCTGGAGTATTTCACCGCCCTAGGCATGATCTACACCGTGGGATCTCCATGTCTCT 128
DB 537 TGAACGGAGGTGTTTACCGCCCTGGGCATGATTTACCGTGGGCTACTCCGTGTCCT 596
QY 129 CGCTCCCTCACGGTGGCTGTGCTCATCTGGCCATATTTAGGCGGTGCACTGCACGCG 188
DB 597 GCGTCCCTCACCGTAGCTGTGCTCATCTGGCCATATTTAGGCGGTGCACTGCACGCG 656
QY 189 CAATACATCAATGACATGTTTCCTGTGTTATGCTGGGCGCCGAGCATCTTCGT 248
DB 657 CAATACATCAATGACATGTTTCCTGTGTTATGCTGGGCGCCGAGCATCTTCGT 716
QY 249 GAAGGACGCTGTGCTCTACTCTGCTTTCAGCTGGATGAGCGCGGCTTCACAGAGGA 308
DB 717 CAAGGACGCTGTGCTCTACTCTGCGCCACGCTTGATGAGGCTGAGCGCCTCACCGAGGA 776
QY 309 AGAGTTGCATCATCGCGAGGTGCCACCTTCGCGCGCGCTGCGCGCGTAGGCTACGC 368
DB 777 GAGCTGGCGCCATCGCCAGGCGCCCGCGCGCTGCCACGCGCGCTGCGCGCTAGCG 836
QY 369 TGGCTGCGCGGTGGCGGTGACCTTCTCTCTACTCTCTGCTGCTACCACTACTAGTAT 428
DB 837 GGGTGCAGGCTGTGCTGACCTTCTCTCTACTCTCTGCTGCTGCGCCACCACTACTAGT 896
QY 429 CCTGGTGGAGGGGTGTACTTTCACAGCCTCATCTTCATGCGCTTTTCTCAGAGAAGAA 488
DB 897 TCTGGTGGAGGGGTGTACTTTCACAGCCTCATCTTCATGCGCTTTTCTCAGAGAAGAA 956
QY 489 GTACTGTGGGGCTTTCACCATCTTGTGGGTGGGTCTACCGGCTGTCTTCGGCTGTGTG 548
DB 957 GTACTGTGGGGCTTTCACAGTCTTCGGGTGGGTCTGCGGCTGTCTTCGGTGGGTGTG 1016
QY 549 GGTGGTGTGACGACAACTTGGGCAACACTGGGTGTGGATCTGGATCTCGGGACAA 608
DB 1017 GGTGAGTGTGACGACAACTTGGGCAACACTGGGTGTGGATCTGGATCTCGGGACAA 1076
QY 609 GAACTGGATCATCCAGGTGCCCTCCTGGCATCTGTTGTGCTCAACTTCATCTCTTTTAT 668

DB 1077 AAGTGGATCATCCAGTGGCCCATCTGGCTCAATTGTGCTCAACTTCATCTCTTCAT 1136
QY 669 CAACATCATCCGGGTGCTGCTAAGCTTCGGGAGACCAATGCGGCGCGGTGTGACAC 728
DB 1137 CAATATCGTCCGGGTGCTGCTGCCACCAAGCTCGGGAGACCAACCGCGCGGTGTGACAC 1196
QY 729 CAGGACGAGTACCGGAAGCTGCTCAGGTCCAGGTTGGTGTGCTGCTGCGCTCTTTGGTGT 788
DB 1197 ACGGACGAGTACCGGAAGCTGCTCAATTCACGCTGGTGTGCTCATGCCCTCTTTGGCGT 1256
QY 789 GCACTACACCGTCTTCATGGCCCTTGCCGTACACCGAGGTCTCAGGAGCAATTTGGGAGAT 848
DB 1257 CCACTACATTGCTCTTCATGGCCACCAATACCGAGGTCTCAGGAGCGCTCTGGCAAGT 1316
QY 849 CAGATGCAATATGAGATGCTCTTCAACTCTTCAGGGATTTTTTTGTTGCGCATCATATA 908
DB 1317 CCAGATGCACTATGAGATGCTCTTCAACTCTTCAGGGATTTTTTTGTTGCGCATCATATA 1376
QY 909 CTGTTTCTGCAATGTTGAGTGCAGGAGGATTTAGGAAGTATGAGAGCGCGCTGGACACT 968
DB 1377 CTGTTTCTGCAATGTTGAGGATCAAGCTGAGATCAAGAAATCTTGGAGCGCTGGACACT 1436
QY 969 GCGTTTGGACTTCAAGCGCAAAACGCAAGTGGGAGTAGCAGCTACAGCTATAGCTACGCGCCCAT 1028
DB 1437 GGCATGGACTTCAAGGGAAGGACGACGAGGAGCAGCAGCTATAGCTACGCGCCCAT 1496
QY 1029 GGTGTCTCACAGTGTGACCAATGTGGGCGCCCGCTGCAAGGACTCAGGCTCCCGCTCAG 1088
DB 1497 GGTGTCCCAACAAAGTGTGACCAATGTGGGCGCCCGCTGTTGGGACTCGGCGCTCAG 1556
QY 1089 CCCCSCG---CTGCTCTGCGCACTACCAATGGCCACTCCAGCTGCTGGGCCATGCCAA 1145
DB 1557 CCCCSCGCTACTCCCACTGCGCACTACCAAGCGCCACCTCAGCTGCTGGGCCATGCCAA 1616
QY 1146 GCAGGGGGTCCAGCCACTGAGAC---TGAAACCTTACCAAGTCACTATGCGGTTCCTCAA 1202
DB 1617 GCCAGGAGCCCGAGCCCTGGAGACCTCGAGACCAACACCACTGCTGCTGCCAA 1676
QY 1203 GGAAGTGGATTCCTTAAAGGCTCTGCTCAGGCGCTGGATGAGGAGGCTCCCGGTGTC 1262
DB 1677 GGAAGTGGGTTCCTCAAGGCTCTGCTCAGGCGCTGGAGGAGGCTCTGGGCGCTGA 1736
QY 1263 GCGGCGCGCTCCATTTGTCAGGAAGATGGGAAACAGTCAATG 1305
DB 1737 GCGGCGCGCTGCTGCTCAGGAAGTGGGAGAGTCAATG 1779

RESULT 15

US-09-943-446-1
; Sequence 1, Application US/09943446
; Patent No. US2002014677A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2177
; TYPE: DNA
; ORGANISM: Canine
US-09-943-446-1
Query Match 68.3%; Score 902.2; DB 9; Length 2177;

Best Local Similarity 84.0%; Pred. No. 2.2e-265; Matches 1066; Conservative 0; Mismatches 173; Indels 30; Gaps 3;			
Qy	69	TGCGTGGAGGATATTTGACCGCCTAGGCAATCTACACCGTGGGATACCTCATGTCTCT	128
Db	802	TGACGGGAGGTGTTGACCGCCTGGGCAATCTACACCGTGGGCTACTCCGTGTGCT	861
Qy	129	CGCTCCCTCAAGTGGGTGCTGCTATCTCTGGCTATTTTAGGCGGTGCACTGCACGCG	188
Db	862	GGCTCCCTCAAGTGGGCGGTGCTATCTGGCTTACTTACGGCGGTGCACTGCACACG	921
Qy	189	CAACTACATCACATGACATGTTCTGTCTGCTTATGCTGCGCGCGGAGCATCTTCGT	248
Db	922	CAACTACATCACATGACATGTTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	981
Qy	249	GAAGGAGCGTGTGCTTACTTCTGCTTTCACGCTGGATGAGCGCGGCTTACAGAGGA	308
Db	982	CAAGGACGGGTGCTTACTTGGGGCCACGCTCGACGAGCGCGCTTACGGAGGA	1041
Qy	309	AGATTGCAATCATGCGGAGGTGCCACCTCCGCGCGCGCTCCGCGGTAGGCTACGC	368
Db	1042	AGAGTGGCGCCATCGCCACG---CACCCCGCGCGCCACCGCGCGCGGCTACGC	1098
Qy	369	TGGCTGCGCGTGGGGTGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	428
Db	1099	GGGCTGCAGGGTAGCTGTGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1158
Qy	429	CCTGCTGAGGGGCTGTACTTGCACAGCCTCATCTTCTATGGCCTTTTCTCAGAGAAGAA	488
Db	1159	TCTGCTGAGGGGCTGTACTTGCATAGTCTCATCTTCTATGGCCTTCTTCTCAGAGAAGAA	1218
Qy	489	GTACTGTGGGGTTACCACTTTTGGCTGGGGTCTACCGGCTGCTTCTTCTGCTGTGTG	548
Db	1219	GTACTGTGGGGTTACCGCTTTCGGCTGGGGTCTGCGCGCGCTTCTTCTGCTGTGTG	1278
Qy	549	GGTGGGTGACAGCAACCTTGGGCAACACTGGGCTGTGGGCTGTAGCTCCGGGACAA	608
Db	1279	GGTCAAGGTGAGAGCCACCTTGGGCAACACTGGGCTGTGGGCTGTAGCTCCGGGACAA	1338
Qy	609	GAAGTGGATCATCAGGTGCCCATCTTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGG	668
Db	1339	GAAGTGGATCATCAGGTGCCCATCTTGGGCTGTGGGCTGTGGGCTGTGGGCTGTGGG	1398
Qy	669	CAACATCATCGGGTGTGCTTACCTAAGCTTCGGGAGACCAATCGGGCGGGTGTGACAC	728
Db	1399	CAACATCGTCCGGTGTGCTCGCCACCAAGTTCGGGAGACCAATCGGGCGGGTGTGACAC	1458
Qy	729	CAGGACAGGTACCGGAGCTGTGCTCAGGTCAAGTGTGGTGTGCTGCTGCGGCTCTTTGGTGT	788
Db	1459	CAGGACAGGTACCGGAGCTGTGCTCAATCCACACTGGTGTCTATGCGGCTCTTTGGGCT	1518
Qy	789	GCACTACACGCTCTTCTATGGCTTGGGCTTACCGGAGTCTCAGGGACATTTGTGGCAGAT	848
Db	1519	CCACTACATGCTCTTCTATGGGACGCGGTACCGGAGTCTCAGGGAGCTCTGGCAAGT	1578
Qy	849	CCAGATGCATTTATGAGATGCTCTTCAACTCTCTCCAGGATTTTTTGTGGCATCATATA	908
Db	1579	CCAGATGCATTTATGAGATGCTCTTCAACTCTCTCCAGGATTTTTTGTGGCATCATATA	1638
Qy	909	CTGTTTCTGCAATGGTGAAGTGCAGGAGAGATTTAGGAAGTGCAGGAGCGCTGGACACT	968
Db	1639	CTGTTTCTGCAATGGGAGGTACAGGCGCGAGATCAAGAAATCTCTGGAGCGGCTGGACACT	1698
Qy	969	GGCGTGGACTTCAAGCGCAAGCACGAAGTGGGAGTAGCAGCTACAGCTATGGCCCAAT	1028
Db	1699	GGCGTGGACTTCAAGCGCAAGCGCCGAAGTGGGAGCAGAGTTACAGCTACGGCCCGAT	1758
Qy	1029	GGTGTCTCACAGAGGTGACCAATGTGGGCGCCCGTGCAGGACTCAGCCTCCCGCTCAG	1088
Db	1759	GGTGTCTCACAGAGGTGACCAATGTAGGCGCCCGGCGGAGCTTGGGCTGCGGCTCAG	1818
Qy	1089	CCCCCGGCTGC-----CTCTGTGCCACTACCAATGGCCACTCCCA	1127

Search completed: July 4, 2005, 06:09:21
Job time : 2716 secs

Db	1819	CCCCCGCCTGTGCTGCCCGCCCTGCCGCCACACACCGCCACCAACCGGCCACCCCC	1878
Qy	1128	GCTGCTTGGCCATGCCAAGCCAGGGGCTCCAGGCCACTGAGACTGAAACCTTACCAGTCAC	1187
Db	1879	GATCCCGGGCCACACCAAGCCAGGGGCCCGGCCCTCCCG-----GCCACACCACTGC	1932
Qy	1188	TATGGCGGTTCCCAAGGACGATGGATTCTTTAAGGGCTCTGCTCAGGCTTGGATGAGGA	1247
Db	1933	CACGGCTGTCTCCCAAGGACGATGGGTTCTTCAACGGCTCTGCTCGGGGCTGGACGAGGA	1992
Qy	1248	GGCTCCGGGTCTGCGCGCGGCTCCATTTGTTGACGGAAGGATGGGAAACAGTCATGTG	1307
Db	1993	GGCTCCGGCGCGGAGCGGCTCCCGCCCTGCTGCAGGAGAGTGGGAGCGGTCTGTG	2052
Qy	1308	ACTGGGCAC	1316
Db	2053	ATCGGGAC	2061

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2005, 23:04:09 ; Search time 4770 Seconds
(without alignments)
10533.509 Million cell updates/sec

Title: US-09-869-565-1

Perfect score: 1320

Sequence: 1 atgggggcccgcggatcgc.....tcattgtactgggcaactagg 1320

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	844.4	64.0	2090	3	BC031578 Homo sapi
2	839.8	63.6	2009	3	CR595263 full-leng
3	816.8	61.9	1701	9	AV398834 Mus muscu
4	762.6	57.8	929	6	CB183774 AGENCOURT
5	732	55.5	905	4	BG972488
6	714.2	54.1	876	4	BI102266
7	703.2	53.3	1037	5	BX381740
8	674.8	51.1	1707	9	AV398832 Homo sapi
9	661.4	50.1	808	7	CK595861
10	657.4	49.8	838	7	CK598594
11	657.4	49.8	1035	5	BQ072459
12	650	49.2	949	2	BF789775
13	642.6	48.7	710	6	CB600301
14	629.8	47.7	751	6	CA945951
15	622.2	47.1	765	4	BG970555
16	613.8	46.5	667	1	AA575668
17	603	45.7	927	6	CB181376
18	595.8	45.1	1051	7	CK231618
19	591.2	44.8	767	7	CO569702
20	581.8	44.1	827	1	AA987157
21	581.6	44.1	944	6	CB203544
22	576.8	43.7	713	6	CB322650
23	576.8	43.7	739	7	CK474354
24	568.2	43.0	897	2	BF780184

C 25	546.6	41.4	553	2	BE101119
C 26	529	40.1	653	5	BQ191730
C 27	522.8	39.6	701	1	AI327170
C 28	519.4	39.3	638	6	CA508167
C 29	512.2	38.8	517	1	AI409036
C 30	511.8	38.8	539	5	BQ552052
C 31	508.8	38.5	662	6	CA508789
C 32	502.4	38.1	1647	2	BF782971
C 33	496.2	37.6	808	7	CV078279
C 34	486	36.8	952	4	BG828526
C 35	456.8	34.6	556	2	BE749381
C 36	456.8	34.6	1707	9	AV398833
C 37	447	33.9	898	5	BQ219643
C 38	444	33.6	456	2	BE115534
C 39	442.4	33.5	540	2	BE749383
C 40	439.6	33.3	542	2	BE014986
C 41	436.4	33.1	554	1	AA240746
C 42	436	33.0	786	7	CO959840
C 43	432.2	32.7	571	5	BQ190700
C 44	429.6	32.5	763	7	CO893473
C 45	429.4	32.5	925	4	BF980406

ALIGNMENTS

RESULT 1	BC031578	2090 bp	mRNA	linear	HTC 01-APR-2004
LOCUS	BC031578				
DEFINITION	Homo sapiens parathyroid hormone receptor 1, mRNA (cDNA clone IMAGE:5180885), with apparent retained intron.				
ACCESSION	BC031578				
VERSION	BC031578.1	GI:21618747			
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2090)				
AUTHORS	Klausner, R.D., Collins, F.S., Wagner, L.H., Shennen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heien, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences (2002)				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99	(26)	16899-16903	(2002)
PUBMED	12477932				
REFERENCE	2 (bases 1 to 2090)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NTH-MGC project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgapbs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc.				

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 50 Row: b Column: 11
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4506270
 This clone has the following problem: retained intron.

FEATURES

source

1. 2090
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:518085"
 /tissue type="Brain, Lung, Testis, adult, pooled whole"
 /clone lib="NIH MGC_115"
 /lab host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 64.0%; Score 844.4; DB 3; Length 2090;
 Best Local Similarity 82.3%; Pred. No. 9.7e-207;
 Matches 1035; Conservative 0; Mismatches 156; Indels 67; Gaps 3;

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Db 800 GGGTCCCTCACCAGTAGTGTGCTCATCTGGCCCTACTTTAGGGGGCTGCACTGCACGCG 859
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Qy 249 GAAGGAGCTGTGCTACTCTGCTTCACTGCTGATGAGCGGAGCGCTCAGAGGA 308
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Db 1040 GGGCTGCGAGGTGCTGTGACCTTCTTCTTACTTCTTGGCCACCAACTACTACTGGAT 1099
Qy 429 CTTGTTGAGGGGTGCTACTGTCAGAGCTCATCTTATGCGCCCTTTTCTCAGAGAGAA 488
Db 1100 TCTGTTGAGGGGTGCTACTGTCAGAGCTCATCTTATGCGCCCTTCTTCTCAGAGAGAA 1159
Qy 489 GTACTGTGGGGCTTACCATCTTTTGGCTGGGGCTACCGGCTGCTTGGGGCTGTGTG 548
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Db 1190 -----GGGTGCTGGGACTTGGATCTGGGAGAA 1218
Qy 609 GAAGTGTATCATCAGGTGCCATCTCGGATCTGTTGCTCAACTTCATCTTTTAT 668
Db 1219 AAAGTGTATCATCAGGTGCCATCTCGGCTCCATTTGTGCTCAACTTCATCTTTTAT 1278
Qy 669 CAACATCATCCGGGTGCTTGCCACTAAGCTTCGGGAGACCAATCGCGGCGGTGTGACAC 728

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Db 1279 CATATCGTCCGGGTGCTGCCACCAAGCTGCGGAGACCAACGCGCGCGGTGTGACAC 1338
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Db 1339 ACGGAGAGTACCGGAAGCTGCTCAAAATCCAGCTGGTCTCATGCGCCCTCTTTGGCGT 1398
Qy 789 GCACTACACCGTCTTCATGCGCTTCCGTACACCGAGGTCTCAGGAGCATTTGTGGCAGAT 848
Db 1399 CCATCATTTGCTTATGCGCCACACCATACACGAGGTCTCAGGAGCGCTTGGCAAGT 1458
Qy 849 CCAGATGCATTATGAGATGCTCTTCAACTCTCTCCAGGGATTTTGTGCGCATCATATA 908
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Qy 909 CTGTTCTTGAATGTTGAGGTGAGGAGGATAGGAAGTCAATGAGGCGCTGGACACT 968
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Qy 1263 GCGGCGCGCTTCAATTTGTCAGGAGATGGGAAACAGTCACTGATGCGGCACTAGG 1320
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RESULT 2

CR595263

LOCUS

DEFINITION CR595263 2009 bp mRNA linear HTC 21-JUL-2004
 full-length cDNA clone CS0D1069YC10 of Placenta Cot 25-normalized
 of Homo sapiens (human).

ACCESSION

CR595263

VERSION

CR595263.1

KEYWORDS

HTC; CNSLUT_cDNA.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 2009)

AUTHORS

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished

REMARK

Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600

REFERENCE

2 (bases 1 to 2009)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a

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division of Invitrogen.
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Query Match       63.6%; Score 839.8; DB 3; Length 2009;
Best Local Similarity 87.4%; Pred. No. 1.5e-205;
Matches 919; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 69 TGCCTGAGGATATTTGACCGCTAGGACATGATCTACACCGTGGGATACTCCATGCTCT 128
Db |||||
Qy 870 TGAACGGGAGGTGTTGACCGCTGGGATGATTTACACCGTGGGCTACTCCGCTGCTCT 929
Db |||||
Qy 129 CGCTCCCTACGGTGGCTGCTGCTATCTGCTGCTATCTGCTGCTATTTAGGCGGCTGCACTGACGG 188
Db |||||
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Db |||||
Qy 309 AGAGTTGACATATCGCGAGGTGCCACCTCCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 368
Db |||||
Qy 1110 GGAGCTGCGGCCATCGCCAGGCGCCCGCGCGCTGCCACCGCGCTGCGCGCTACGC 1169
Db |||||
Qy 369 TGGCTGCGCGTGGCGGTGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 428
Db |||||
Qy 1170 GGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1229
Db |||||
Qy 429 CTTGCTGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 488
Db |||||
Qy 1230 TCTGCTGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1289
Db |||||
Qy 489 GTACCTGTTGGGGCTTACCAATCTTTGGCTGGGGCTTACCGGCTGCTGCTGCTGCTGCTGCTGCTG 548
Db |||||
Qy 1290 GTACCTGTTGGGGCTTACCAATCTTTGGCTGGGGCTTACCGGCTGCTGCTGCTGCTGCTGCTGCTG 1349
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Qy 549 GGTGCTGTTGAGCAACCTTGGGCAACACATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 608
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Qy 1350 GGTGAGTGTGAGAGCTTACCTGGGCAACACCGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1409
Db |||||
Qy 609 GAAGTGGATCATCCAGGTGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
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Qy 1410 AAAGTGGATCATCCAGGTGCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1469
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Qy 669 CAACATCATCCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
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Qy 1470 CAATATCGTCCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1529
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Qy 789 GCATGTACACGCTTTCATGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 848
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Qy 1590 CCATGTACATGCTTTCATGGCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1649
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Qy 849 CCAGATGATATGAGATGCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 908
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[illegible]

CB183774	929 bp	mRNA	linear	EST 31-JAN-2003
LOCUS	AGENCOURT 11384721 NIH MGC 164	Mus musculus	cDNA clone	
DEFINITION	IMAGE:30244792 5', mRNA sequence.			
ACCESSION	CB183774			
VERSION	CB183774.1	GI:28182891		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1. (bases 1 to 929)			
TITLE	NIH-MGC http://mgi.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-1@mail.nih.gov Tissue Procurement: Dr. David Rowe and Dr. Mina cDNA Library Preparation: Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDAM0318 row: d column: 17 High quality sequence start: 2 High quality sequence stop: 590.			
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	/clone="IMAGE:30244792"			
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ORIGIN				
Query Match	57.8%;	Score 762.6;	DB 6;	Length 929;
Best Local Similarity	95.5%;	Pred. No. 1.1e-185;		
Matches	807;	Conservative 0;	Mismatches 34;	Indels 4; Gaps 2;
Qy	73	CTGGAGGTATTACCGCCTAGGCATGATCTACACCGTGGGATCTCCATGTCTCTCGCC	132	
Db	85	CGGAGGTATTACCGCCTGGGCATGATCTACACCGTGGGATTCATGTCTCTTGGC	144	
Qy	133	TCCCTCACGCTGGCTGTGCTCATCTCGCCTATTTTAGCGGGTGTCACTGCACGCGCAAC	192	
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Db	205	TACATCCACATGCACATGTTCTGTGCTTTATGTGCGCGCGCGAGCATCTTCGTGAAG	264	
Qy	253	GACGCTGTGCTTACTCTGGCTTCACGCTGGATGAGCCGAGCGCCTCACAGAGGAGAG	312	
Db	265	GACGCTGTGCTTACTCTGGCTTCACGCTGGATGAGCCGAGCGCCTCACAGAGGAGAG	324	
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Db	325	TTGCATATCATCGCGAGGTGGCGCCTTCGCGCGCGCTGCGCGCGTAGGCTAGCGTGGC	384	
Qy	373	TGCGCGTGGCGGTGACCTTCTTCTCTACTTCTTGGCTACCAACTACTTGGATCTGT	432	
Db	385	TGCGGTGGCGGTGACCTTCTTCTCTACTTCTTGGCTACCAACTACTTGGATCTGT	444	

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QY 433 GTGAGGGGCTGTACTTCACAGCCTCATCTTCAATGCGCTTTTCTCAGAGAAGATGAC 492
Db 445 GTGAGGGGCTGTACTTCACAGCCTCATCTTCAATGCGCTTTTCTCAGAGAAGATGAT 504
QY 493 CTGTGGGCTTCCACCATCTTGGCTGGGGTCTACCGGCTGTCTCGTGGCTGTGGGTC 552
Db 505 CTGTGGGCTTCCACCATCTTGGCTGGGGTCTACCGGCTGTCTCGTGGCTGTGGGTC 564
QY 553 GGTGTACAGCAACCTTGGCCAAACATCTGGGTGCTGGGATCTGAGCTCCGGSCACAGAAG 612
Db 565 GGTGTACAGCAACCTTGGCCAAACATCTGGGTGCTGGGACCTGAGCTCTGGSCACAGAAG 624
QY 613 TGGATATCCAGGTGCGCCATCTGTCATCTGTGTGCTCAACTCTTCTTATCAAC 672
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Db 805 TACACCGTCTTATGAGGCTTCCGCTTACACCGAGGTCTCAGGACATTTG-TGGCAGATCCA 864
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QY 909 CTGTT 913
Db 925 CTGGT 929

RESULT 5
LOCUS BG972488
DEFINITION BG972488.1 NC1_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4975671
5', mRNA sequence.
ACCESSION BG972488
VERSION BG972488.1 GI:14360125
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 905)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M10967 row: m column: 16
High quality sequence stop: 841.
Location/Qualifiers
1..905
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FEATURES
source
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/clone_lib="NC1_CGAP_Kid14"
/notes="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NC1_CGAP Library. |"
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ORIGIN

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Query Match 55.5%; Score 732; DB 4; Length 905;
Best Local Similarity 92.4%; Pred. No. 8.8e-178;
Matches 837; Conservative 0; Mismatches 60; Indels 9; Gaps 6;

QY 395 TCCTCTACTTCCCTGGCTACCAACTACTACTGATCTCTGAGGGGCTGTACTTTGACACA 454
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QY 455 GCCTCATCTTTCATGGCCCTTTTCTCAGAGAAGATGATCTGTGGGGCTTCAACCATCTTTG 514
Db 61 GCCTCATCTTTCATGGCCCTTTTCTCAGAGAAGATGATCTGTGGGGCTTCAACCATCTTTG 120
QY 515 GTGGGGTCTTACCGGCTGTCTTGTGTGTGGGTGCGGTGTGAGAACACCTTGTGCGCA 574
Db 121 GTGGGGTCTTACCGGCTGTCTTGTGTGTGGGTGCGGTGTGAGAACACCTTGTGCGCA 180
QY 575 ACATGGGTCTGGGATCTGAGCTCCGGGACAGAGATGATCATCAGGTGGCCATCC 634
Db 181 ACATGGGTCTGGGATCTGAGCTCCGGGACAGAGATGATCATCAGGTGGCCATCC 240
QY 635 TGGCATCTGTGTGCTCAACTTTCATCTTTCATCAACATCATCCGGGTGTGCGCACTA 694
Db 241 TGGCATCTGTGTGCTCAACTTTCATCTTTCATCAACATCATCCGGGTGTGCGCACTA 300
QY 695 AGCTTCCGGAGACCAATGCGGGCGGTGTGACACAGGAGAGTACCGGAAGTGTGCA 754
Db 301 AGCTTCCGGAGACCAATGCGGGCGGTGTGACACAGGAGAGTACCGGAAGTGTGCA 360
QY 755 GGTCCACGTTGTGCTGTGCGGCTCTTGTGGTGTGACTACCGCTTTCATGCGCTTGC 814
Db 361 GGTCCACGTTGTGCTGTGCGGCTCTTGTGGTGTGACTACCGCTTTCATGCGCTTGC 420
QY 815 CGTACACCGAGGTCTCAGGAGACATTTGGCAGATCCAGATGTCATTTAGAGATGCTTTCA 874
Db 421 CGTACACCGAGGTCTCAGGAGACATTTGGCAGATCCAGATGTCATTTAGAGATGCTTTCA 480
QY 875 ACTCTTCCAGGATTTTGTGTCATATATATCTTTTTCGCAATGAGTGTGAGTGCAGG 934
Db 481 ACTCTTCCAGGATTTTGTGTCATATATATCTTTTTCGCAATGAGTGTGAGTGCAGG 540
QY 935 CAGAGATTAGAAAGTATGAGCGGCTGGGACACTGGCGTTGGACTTCAAGGCGAAGCAC 994
Db 541 CAGAGATTAGAAAGTATGAGCGGCTGGGACACTGGCGTTGGACTTCAAGGCGAAGCAC 600
QY 995 GAAAGTGGGAGTAGCAGCTACAGCTATGCGCCCAATGGTGTCTCACACAGGTGTGACCAATG 1054
Db 601 GAAAGTGGGAGTAGCAGCTACAGCTATGCG-CAATGGTGTCTCACACAGGTGTGACCAATG 659
QY 1055 TGGGCCCCCGTGCAGGACTCAGCCTCCCTTCAGCCCCCGCTGCTCTCTGCTGCTACCA 1114
Db 660 TGGGCCCCCGTGCAGGACTCAG-CTTCCCTTAGCTCCCGCTGCTCTCTGCTGCTGCTC 716
QY 1115 ATGGCCACTCCAGCTGCTGCGCATGCGCAAGCCAGGCGCTCCAGCCACTG-AGACTGAA 1173
Db 717 ATGGCCACTCCAGCTGCTGCGCATGCGCAAGCCAGGCGCTCCAGCCACTGTTGAAGACGA 776
QY 1174 ACCTTACAGTCACTATGGCGGTTCCTCC-AAGGAGATGAGTATCTTAAACGCTCTCTGCTC 1232
Db 777 ACCTTACAGTCACTATGAGCAGTTCCTCCAAAGGAGCAGCGGTCTCTTAAATGGCTCTGCTC 836
QY 1233 AGGCTCTGG---ATGAGGAGGCTCCCGGCTGTGCGCGCGCTCCATTTGTTGACGAGG 1289
Db 837 GGGTCTGGGATGAAGGAGGCTCTTGGGTGGCGGCGCAACCTCCATTTGTTGCGGGAAGA 896
QY 1290 ATGGGA 1295
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```
Db      897 TGGGCA 902

RESULT 6
BI102266
LOCUS   602885578F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5040931
DEFINITION
5', mRNA sequence.
ACCESSION BI102266
VERSION   BI102266.1 GI:14553159
KEYWORDS EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 876)
          NIH-MGC http://mgi.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Jeffrey E. Green, M.D.
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLML at:
          http://image.llnl.gov
          Plate: LLAM1112 row: 1 column: 20
          High quality sequence stop: 790.

FEATURES             source
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            /mol_type="mRNA"
            /strain="FVB/N"
            /db_xref="taxon:10090"
            /clone="IMAGE:5040931"
            /lab_host="DH10B (T1 phage-resistant)"
            /clone_lib="NCI_CGAP_Kid14"
            /note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
            Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.75 kb. Constructed by Life
            Technologies. Note: this is a NCI_CGAP Library. |"

ORIGIN
Query Match      54.1%; Score 714.2; DB 4; Length 876;
Best Local Similarity 92.4%; Pred. No. 3.5e-173;
Matches 807; Conservative 0; Mismatches 58; Indels 8; Gaps 5;

Qy      73 CTGAGGATTTTGACCGCGCTAGGCGATGATCTACACCGTGGGATACCTCCATGCTCTCTCGCC 132
Db      |
Db      7 CGGGAGGATTTTGACCGCGCTAGGCGATGATCTACACCGTGGGATATTCATGCTCTCTCGCC 66
Qy      133 TCCCTCAGCGTGGCTGTGCTCATCTCGGCTATTTTAGCGGCTGCACTGCACGCGCAAC 192
Db      |
Db      67 TCCCTCAGCGTGGCTGTGCTCATCTAGGCTATTTTAGCGGCTGCACTGCACGCGCAAC 126
Qy      193 TACATCACAATGCAATGTTCTGCTGTTTATGCTGCGCGCGCGGAGCAATCTTCTGTAAG 252
Db      |
Db      127 TACATCACAATGCAATGTTCTGCTGTTTATGCTGCGCGCGCGGAGCATCTTCTGTAAG 186
Qy      253 GACGCTGTGCTACTCTGCTGCTTACGCTGATGAGCGCGGCGCTCACAGAGGAAGAG 312
Db      |
Db      187 GACGCTGTGCTACTCTGCTGCTTACGCTGATGAGCGCGGCGCTCACAGAGGAAGAG 246
Qy      313 TTGCACATCATCGCGGAGTGCCACCTCCGCGCGCGCTGCGCGGCTAGGCTAGCTGGC 372
Db      |
Db      247 TTGCATATCATCGCGGAGTGCGCGCTCACCGCGCGCTGCGCGGCTAGGCTAGCTGGC 306
Qy      373 TGCGCGTGGCGGTGACCTTCTTCTGCTACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 432
Db      |
Db      307 TGCGCGTGGCGGTGACCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 366
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433 GTGAGGGGCTGTACTTGCACAGCCTCATCTTCATGGCCCTTTTCTCAGAGAAGAGTAC 492
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367 GTGAGGGGCTGTACTTGCACAGCCTCATCTTCATGGCCCTTTTCTCAGAGAAGAGTAT 426
|
|
|
493 CTGTGGGGCTTCAACATCTTTTGGCTGGGGGTCTACCGGCTGCTTCGTGGCTGTGTGGGTC 552
|
|
|
427 CTGTGGGGCTTCAACATCTTTTGGCTGGGGGTCTGCGGCTGCTTCTCGTGGCTGTGTGGGTC 486
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|
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553 GGTGTGAGAGCAACCTTGGCCACACCTGGGTGCTGGGATCTGAGCTCGGGGCAACAAG 612
|
|
|
487 GGTGTGAGAGCAACCTTGGCCACACCTGGGTGCTGGGATCTGAGCTCTGGGCAACAAG 546
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|
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613 TGGATCATTCAGGTGGCCATCTTGGCATCTGTTGTGCTCAACTTCATCTTTTATCAAC 672
|
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|
547 TGGATCATTCAGGTGGCCATCTTGGCATCTGTTGTGCTCAACTTCATCTTTTATCAAC 606
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|
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673 ATCATCGGGTGTCTGCGCACTAAGCTTTCGGAGACCAATTCGGGCGGCTGTGACACAGG 732
|
|
|
607 ATCATCGGGTGTCTGCGCACTAAGCTTTCGGAGACCAATTCGGGCGGCTGTGACACAGG 666
|
|
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733 CAGCATGACCGAAGCTGCTCAGGT--CCAGTGTGGTCTGCTGCGGCTCTTGTGTGCA 791
|
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667 CAGCATGACCGAAGCTGCTCAGGTCCAGGTGGTGTGCTGTCCTCTTCGGGTGCTCA 726
|
|
|
792 CTACACCC--GTCTTTCATGGCTTGGCTACACCGAGGTCTCAGGGACA--TTGTGGCAGA 847
|
|
|
727 CTACACCCGTCTTTCATGGCTTGGCTACACCGAGGTCTCAGGGACACCTGTGGCAGA 786
|
|
|
848 TCAGATGCAATATGAGATGCTCTTCAACTCTCTTCAGGGATTTTGTGGCATCATAT 907
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|
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787 TCAGATGCAATATGAGATGCTCTTCAACTCTCTTCAGG--ATTTTTGTGGCATCATAT 844
|
|
|
908 ACTGTTTCTGCAATGCTGAGGTGCAGGCAGAGA 940
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845 AC-GGTTCTGCAAGGTGAAGGTGCGGGAAATA 876

RESULT 7
BX381740/c
LOCUS   BX381740 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION
clone CSODI069YC10 3-PRIME, mRNA sequence.
ACCESSION BX381740
VERSION   BX381740.2 GI:46833542
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1037)
          Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
          Full-length cDNA libraries and normalization
          Unpublished (2001)
          On May 8, 2003 this sequence version replaced gi:30458988.
          Contact: Genoscope
          Genoscope - Centre National de Sequencage
          2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
          Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
          1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen. This sequence belongs to sequence cluster
          2183.r
          For more information about this cluster, see
          http://www.genoscope.cns.fr/cdna?s=CSODI069BB05NP1&c=2183.r.
          Location/Qualifiers
            1..1037
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
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              /tissue_type="PLACENTA COT 25-NORMALIZED"
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/clone.lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and cloned into the Not I and EcoR V  
sites of the pCWSport 6 vector. Library was normalized."
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ORIGIN

Query Match 53.3%; Score 703.2; DB 5; Length 1037;
Best Local Similarity 85.6%; Pred. No. 2.5e-170;
Matches 810; Conservative 5; Mismatches 128; Indels 3;

Qy	174	GCTGCACTGCACGGCGCAACTACATCCACATGCAATGTTCTGTGCTGTTATGCTGCGGCG	233
Db	1033	GCTGCACTGCACGGCGCAACTACATCCACATGCACTGTCTCCCTGTCTTCCATGCGGCGC	974
Qy	234	CGCGAGCATCTTCGTGAAGGACGCTGTGCTCTACTCTGTGGCTTCACGCTGATGAGGCGGA	293
Db	973	CGTGAGCATCTTCGTGAAGGAGTGTGCTCTACTCT- GCGCCACGCTTGAAGA- GCTGA	916
Qy	294	CGCGCTCACAGAGGAAGTTCACATCATCGCGAGGTGCCACTCGCGCGCGCTGC	353
Db	915	CGCGCTCACCGAGAGGA- CKGCGCGCATGCGCCAGGCGCCCGCGCTGCACCCG	857
Qy	354	CGCGTAGGCTACGCTGGCTGCCGCTGGGGGTGACCTTCCTCTACTTCCTGGGTAC	413
Db	856	CGCGTGCAGGTACGCGGGCTGCAGGGTGGCTGTGACCTTCCTCTTACTTCCTGGCCAC	797
Qy	414	CAACTACTACTGGATCTCTGTGTGAGGGGCTGTACTTGTGCAAGCCTCATCTTCATGGGCTT	473
Db	796	CAACTACTACTGGATCTCTGTGTGAGGGGCTGTACTCTGCACAGCCTCATCTTCATGGGCTT	737
Qy	474	TTTCTCAGAGAAGATACCTGTGGGGCTTCACCATCTTTTGGCTGGGGCTACCGGCTGT	533
Db	736	CTTCTCAGAGAAGATACCTGTGGGGCTTCACAGTCTTGCGCTGGGGCTGCGCCGCTGT	677
Qy	534	CTTCGTGGCTGTGTGGGTCTGGTGTGCAGAGCAACCTTGGCCAACTGGGTGCTGGGACT	593
Db	676	CTTCGTGGCTGTGTGGGTCTAGTGTGCAGAGTACCTTGGCCAACTGGGGTGTGGGACT	617
Qy	594	GAGCTCGGGCAAGAAGTGGATCATCCAGGTGCCCATCTCGTCATCTCTGTGTGCTCAA	653
Db	616	GAGCTCGGGCAACAAAAGTGGATCATCCAGGTGCCCATCTCGTCTCCATCTGTGTCTCAA	557
Qy	654	CTTCATCTCTTTTATCAACATCATCCGGGTGCTGCCACTAAGCTTCGGGAGACCAATGC	713
Db	556	CTTCATCTCTTTCATCAATATCGTCCGGGTGCTGCCCAACCAAGCTGCGGGAGACCAACGC	497
Qy	714	GGGCGGTGTGACACAGGAGCAGTAGTACCGGAAGCTGCTCAGGTCCACGTTGGTCTCGT	773
Db	496	CGGCGGTGTGACACAGGAGCAGTAGTACCGGAAGCTGCTCAATCCACGCTGGTGTCTCAT	437
Qy	774	GCCTCTTTTGGTGTGCACTACACCGTCTTTCATGGCTTGCCTGTCCGTACACCGAGGTCTCAGG	833
Db	436	GCCTCTTTTGGCGTCACTACATTTGTCTTCATGGCCACACCATACACCGAGGTCTCAGG	377
Qy	834	GACATTTGGCAGATCCAGATGCAATATGAGATGCTCTTCAACTCTTCAGGGATTTT	893
Db	376	GAGCTCTGGCAAGTCCAGATGCACTATGAGATGCTCTTCAACTCTTCAGGGATTTT	317
Qy	894	TGTTGCCATCATATATCTGTTTCTGCAATGTGAGGTGAGGCAGAGATTTAGGAAGTCAATG	953
Db	316	TGTGCGCAATCATATATCTGTTTCTGCAACGGCGAGGTACAAGCTGAGATCAAGAAATCTTG	257
Qy	954	GAGCGCTGGACACTGGCGTTTGGACTTTCAGCGCAAGACGAGTGGGAGTAGCAGCTA	1013
Db	256	GAGCGCTGGACACTGGCACTGGGACTTTCAGCGAAAGGCAACGACGGGAGCAGCAGCTA	197
Qy	1014	CAGCTATGGCCCAATGGTGTCTCACAGAGTGTGACCAATGTGGGCCCCCGCTGCAGGACT	1073
Db	196	TAGTACGGCCCAATGGTGTCTCCACACAGATGTGACCAATGTGGGCCCCCGCTGTGGGACT	137
Qy	1074	CAGCCTCCCGCTCAGCCCCCGCGCTGCTCTCTGCCACTACCAATGGC	1119


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|||||
Db 421 AGATGCAATATGAGATGCTCTTCAACCTCTTCCAGGGAATTTTGTGGCAATATATACT 480
Qy 911 GTTTCGCAATGCTGAGTGCAGGACAGAGATTAGGAAGTCAATGAGCGCTGGACACTGG 970
Db 481 GTTTCGCAATGCTGAGTGCAGGACAGAGATTAGGAAGTCAATGAGCGCTGGACACTGG 540
Qy 971 CGTTGGACTTCAAGCGCAAGACAGAAAGTGGAGTAGCAGCTACAGCTATGAGCCCAATGG 1030
Db 541 CGTTGGACTTCAAGCGCAAGACAGAAAGTGGAGTAGCAGCTACAGCTATGAGCCCAATGG 600
Qy 1031 TGTCTCACAGAGTGAACCAATGAGCGCCCGCTGGAGACTCAGCTCCCGCTCAGCC 1090
Db 601 TGTCTCACAGAGTGAACCAATGAGCGCCCGCTGGAGACTCAGCTCCCGCTCAGCC 660
Qy 1091 CCGCGCTGCCTC 1102
Db 661 CCGCGCTGCCTC 672

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RESULT 10
CK598594
LOCUS
DEFINITION
AGENCOURT 17840193 NIH_MGC_238 Rattus norvegicus cDNA clone
IMAGE:7133602 5', mRNA sequence.

CK598594
CK598594.1 GI:41111717
EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 838)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapsb-remail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
<http://image.llnl.gov>
Plate: LLML15037 row: 0 column: 08
High quality sequence stop: 688.

Location/Qualifiers
1..838

FEATURES
source

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/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7133602"
/tissue_type="testis, pooled"
/lab_host="DH10B TONa"
/clone_lib="NIH_MGC_238"
/notes="Organ: testis; Vector: pExpress-1; Site: 1: EcoRV;
Site 2: NotI; RNA obtained from testis tissue of 8 wk old
animal. Tissues were snap-frozen and kept at -80C before
RNA extraction and purification (Tri-reagent method). cDNA
was primed using oligo-dT primer:
5'-pGACTGATCTAGACGAGCGCCGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
resulted in an average insert size of 1.9 kb. This primary
library is normalized (non-normalized primary library is
NIH MGC 237) and was constructed by Express Genomics
(Frédérick, MD)"

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ORIGIN

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Query Match 49.8%; Score 657.4; DB 7; Length 838;
Best Local Similarity 99.7%; Pred. No. 1.6e-158;
Matches 669; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 436 GAGGGGCTGTACTTGCACAGCCTCATCTTCATGSCCTTTTCTCAGAGAAGAGTACTG 495
Db 1 GAGGGGCTGTACTTGCACAGCCTCATCTTCATGSCCTTTTCTCAGAGAAGAGTACTG 60
Qy 496 TGGGGCTTCAACCATCTTTTGGCTGAGGCTTACCGGCTGTCTTCTGTTGGTGTGGTGGT 555
Db 61 TGGGGCTTCAACCATCTTTTGGCTGAGGCTTACCGGCTGTCTTCTGTTGGTGTGGTGGT 120
Qy 556 GTACAGACAACCTTGGCCAACTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGG 615
Db 121 GTACAGACAACCTTGGCCAACTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGG 180
Qy 616 ATCATCCAGGTGCCCATCTCTGGCATCTGTTGTGCTCAACTTTCATCTTTTATCAACATC 675
Db 181 ATCATCCAGGTGCCCATCTCTGGCATCTGTTGTGCTCAACTTTCATCTTTTATCAACATC 240
Qy 676 ATCCGGGTGCTTGCCTAAAGCTTTCGGGAGACCAATCGGGCGGCTGTGACACAGGCGAG 735
Db 241 ATCCGGGTGCTTGCCTAAAGCTTTCGGGAGACCAATCGGGCGGCTGTGACACAGGCGAG 300
Qy 736 CAGTACCGGAAGTGTCTCAGGTTCAGCTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 795
Db 301 CAGTACCGGAAGTGTCTCAGGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 360
Qy 796 ACCGTCTTTCATGCGCTTTCGGTTCACCGAGGTCTCAGGAGCATTTGTGCGAGATCCAGATG 855
Db 361 ACCGTCTTTCATGCGCTTTCGGTTCACCGAGGTCTCAGGAGCATTTGTGCGAGATCCAGATG 420
Qy 856 CATTATGAGATGCTCTTCAACTCTCTTCAGGGATTTTGTGTCATCATATCTGTTC 915
Db 421 CATTATGAGATGCTCTTCAACTCTCTTCAGGGATTTTGTGTCATCATATCTGTTC 480
Qy 916 TGCAATGCTGAGTGCAGGCGAGAGATTAGGAAGTTCATGAGGCGCTGGACACTGGCGTTG 975
Db 481 TGCAATGCTGAGTGCAGGCGAGAGATTAGGAAGTTCATGAGGCGCTGGACACTGGCGTTG 540
Qy 976 GACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCTATGCCCCCAATGGTGTCT 1035
Db 541 GACTTCAAGCGCAAGACCAAGTGGAGTAGCAGCTACAGCTATGCCCCCAATGGTGTCT 600
Qy 1036 CACACGAGTGTGACCAATGTGGCGCCCGCTGCGAGGACTCAGCTCCCGCTCAGCCCCCGC 1095
Db 601 CACACGAGTGTGACCAATGTGGCGCCCGCTGCGAGGACTCAGCTCCCGCTCAGCCCCCGC 659
Qy 1096 CTGCTCTCTGC 1106
Db 660 CTGCTCTCTGC 670

```

RESULT 11
BQ072459
LOCUS

DEFINITION
AGENCOURT 6838764 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5761637
5', mRNA sequence.

ACCESSION
BQ072459
KEYWORDS
EST.

SOURCE
Homo sapiens (human)
Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 1035)
NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS
TITLE
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
JOURNAL
Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.


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Qy 170 GCGGGCTGCACTGACGCGCAACTATCCATGACAT-GTTCCTGTCTTTATGCTG 228
Dy 1 GCGGGCTGCACTGACGCGCAACTATCCATGACATGTTCTGCTGTTATGCTG 60
Qy 229 CGCGCGCGAGCATCTTGTGTAAGGACGCTGCTACTCTGCTTACGCTTACGCTGATGAG 288
Dy 61 CGCGCGCGAGCATCTTGTGTAAGGACGCTGCTACTCTGCTTACGCTTACGCTGATGAG 120
Qy 289 GCCGAGCGCTTCACAGAGAGAGTTGCAATCATCGCGAGAGTCCACCTCCCGCGGCC 348
Dy 121 GCCGAGCGCTTCACAGAGAGAGTTGCAATCATCGCGAGAGTCCCGCTCCACCGGCC 180
Qy 349 GCTCGCGCGTAGGCTACGCTGCTGCGCTGCGCTGCGGTGACCTTCTTCTTACTTCTG 408
Dy 181 GCTCGCGCGTAGGCTACGCTGCTGCGCTGCGGTGACCTTCTTCTTACTTCTTCTG 240
Qy 409 GCTACCAACTACTACTGATTTCTGTTGAGGAGTGTACTTACAGAGCTTCTTCTTCTG 468
Dy 241 GCTACCAACTACTACTGATTTCTGTTGAGGAGTGTACTTACAGAGCTTCTTCTTCTG 300
Qy 469 GCCTTTTCTCAGAGAGAGTACTCTGTGGGCTTCCACATCTTGTGGCTGGGCTTACCG 528
Dy 301 GCCTTTTCTCAGAGAGAGTACTCTGTGGGCTTCCACATCTTGTGGCTGGGCTTACCG 360
Qy 529 GCTCTCTTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588
Dy 361 GCTCTCTTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Qy 589 GATCTGAGCTCCGGGACAGAGTGTATCATCAGGTGCCATCTGCGCATCTGTTGTG 648
Dy 421 GATCTGAGCTCCGGGACAGAGTGTATCATCAGGTGCCATCTGCGCATCTGTTGTG 480
Qy 649 CTCAACTTCTCTTTTATCAACATCATCCGGTGTGCTGCTGCTGCTGCTGCTGCTG 708
Dy 481 CTCAACTTCTCTTTTATCAACATCATCCGGTGTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 709 AATCGCGCGCGGTGTGACACAGGACGAGTACCGGAGTGTGCTGCTGCTGCTGCTG 768
Dy 541 AATCGCGCGCGGTGTGACACAGGACGAGTACCGGAGTGTGCTGCTGCTGCTGCTG 600
Qy 769 CTGCTGCGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 828
Dy 601 CTGCTGCGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 658
Qy 829 TCAGGACATTTGCGCAGATCCAG---TGCAATATGAGATGCTTCAACTCTCTCCAG 885
Dy 659 TCAGGACATTTGCGCAGATCCAGAAATGCTTATGAGATGCTTCAACTCTCTCCAG 718
Qy 886 GGATTTTGTGTCATATATCTGTTTCTGCAATGCTGAGGTGCGAGGACAGATTAGG 945
Dy 719 GGATTTTGTGTCATATATCTGTTTCTGCAATGCTGAGGTGCGAGGACAGATTAGG 778
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RESULT 13
CB600301
LOCUS
DEFINITION CB600301 710 bp mRNA linear EST 03-APR-2003
IMAGE:30311807 5', mRNA sequence.
ACCESSION CB600301
VERSION CB600301.1 GI:29518157
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 710)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
```

cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDCM95 row: 1 column: 24
High quality sequence stop: 636.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clones="IMAGE:30311807"
/lab_host="DH10B (TI-phage-resistant)"
/clone_lib="NIH_MGC_176"
/notes="Organ: kidney; Vector: pDNR-LIB; Site 1: SfiI
(ggcattatggcc); Site 2: SfiI (ggcgcctggcc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-ATTCTAGAGCGCGGCGGACATG-dT(30)NN-3'. Full-length
5'-AAGCAGTGGTATCAAGCGGCGGACATG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

```
Query Match 48.7%; Score 642.6; DB 6; Length 710;  
Best Local Similarity 95.7%; Pred. No. 1e-154;  
Matches 671; Conservative 0; Mismatches 29; Indels 1; Gaps 1;  
Qy 396 CCTCTACTCTCTGCTACCACTACTACTGATCTCTGCTGGAGGGGTGTACTTGCACAG 455  
Dy 3 CCTCTACTCTCTGCTACCACTACTACTGATCTCTGCTGGAGGGGTGTACTTGCACAG 62  
Qy 456 CCTCATCTTATGCGCTTTTCTCAGAGAGAGTACTGTGGGGCTTACCATTCTTGG 515  
Dy 63 CCTCATCTTATGCGCTTTTCTCAGAGAGAGTACTGTGGGGCTTACCATTCTTGG 122  
Qy 516 CTGGGGTCTACCGCTGCTCTTCTGCTGGCTGTGGTGGTGTGCTGAGAGCAACTTGGCCAA 575  
Dy 123 CTGGGGTCTACCGCTGCTCTTCTGCTGGCTGTGGTGGTGTGCTGAGAGCAACTTGGCCAA 182  
Qy 576 CACTGGTGTCTGGGATCTGAGCTCCGGGCAACAGAGTGGATCATCCAGGTGCCATCCT 635  
Dy 183 CACTGGTGTCTGGGATCTGAGCTCTGGGCAACAGAGTGGATCATCCAGGTGCCATCCT 242  
Qy 636 GGCACTGTGTGCTCAACTTTCATCTTTTATCAACATCATCCGGGTGTGCTGCTAA 695  
Dy 243 GGCACTGTGTGCTCAACTTTCATCTTTTATCAACATCATCCGGGTGTGCTGCTAA 302  
Qy 696 GCTTCGGGAGACCAATGCGGGCGGCTGTGACACCGGACGACGTACCGGAGCTGCTCAG 755  
Dy 303 GCTTCGGGAGACCAATGCGGGCGGCTGTGACACCGGACGACGTACCGGAGCTGCTCAG 362  
Qy 756 GTCCACGCTTGGTGTCTGCTGCTGCTCTTGTGTGTGCTTACACCGCTTTCATGGCTTGGCC 815  
Dy 363 GTCCACGCTTGGTGTCTGCTGCTCTTGTGTGTGCTTACACCGCTTTCATGGCTTGGCC 422  
Qy 816 GTACACCGAGGTCTCAGGGACATTTGTGGGACATCCAGATGCATTTATGAGATGCTTCAA 875  
Dy 423 GTACACCGAGGTCTCAGGGACATTTGTGGGACATCCAGATGCATTTATGAGATGCTTCAA 482  
Qy 876 CTCTTTCAGGGATTTTCTGCTGCTATATCTGTTTCTGCAATGCTGCTGCTGCTGCTGCTG 935  
Dy 483 CTCTTTCAGGGATTTTCTGCTGCTATATCTGTTTCTGCAATGCTGCTGCTGCTGCTGCTG 542  
Qy 936 AGAGATTAGGAAGTCTATGAGGCGCTGACACCTGCGGTGTGCACTTCAAGGCGCAAGCAG 995  
Dy 543 AGAGATTAGGAAGTCTTGGAGCGCGCTGGACACTTGGCATTTGCACTTCAAGGCGCAAGCAG 602  
Qy 996 AAGTGGGAGTAGCAGCTTACAGCTATGCGCCCAATGGTGTCTCACAGAGTGTGACCAATGT 1055
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/organism="Mus musculus"
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/lab_host="DH10B (T1 phage-resistant)"
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/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"

ORIGIN

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Query Match      47.1%; Score 622.2; DB 4; Length 765;
Best Local Similarity 93.5%; Pred. No. 2e-149;
Matches 715; Conservative 0; Mismatches 43; Indels 7; Gaps 6;

Qy 149 TGCTCATCTGGCCATTATTAGGC-GGCTGCACCTGCACGGCACTACATCCACATGCAC 207
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Qy 208 ATGTTCTCTGTCGTTTATGCTCGCGCGCGCGAGCATCTTCGTGAAGAGCGCTGTCTCTAC 267
Db 61 ATGTTCTCTGTCGTTTATGCTCGCGCGCGCGAGCATCTTCGTGAAGAGCGCTGTCTCTAC 120

Qy 268 TCTGGCTTCAAGCTGGATGAGCGCGCGCTCACAGAGGAAGATTGCACATCATCGCG 327
Db 121 TCTGGCTTCAAGCTGGATGAGCGCGCGCTCACAGAGGAAGATTGCATATCATCGCG 180

Qy 328 CAGGTGCACTCCGCGCGCGCTCGCGCGCTAGGCTACGCTGCTCGCGCGCGCGGTG 387
Db 181 CAGGTGCGGCTCCACCGCGCGCTCGCGCGCTTGGCTACGCTGCTCGCGCGGTG 240

Qy 388 ACCTTCTCTCTACTTCTGCTTACCACTACTACTGATCTGCTGCTGGAGGGCTGTAC 447
Db 241 ACCTTCTCTCTACTTCTGCTTACCACTACTACTGATCTGCTGCTGGAGGGCTGTAC 300

Qy 448 TTGCACAGCCTCATCTTTCAAGCCCTTTTCTCAGAGGAAGTACCTGTGGGGCTTCACC 507
Db 301 TTACACAGCCTCATCTTTCAAGCCCTTTTCTCAGAGGAAGTATCTGTGGGGCTTCACC 360

Qy 508 ATCTTTGGCTGGGCTGTACCGGCTGTCTTCTGCTGCTGTGGGCTGTGCTGCTGAGAGAAC 567
Db 361 ATCTTTGGCTGGGCTGTGCGGCTGTCTTCTGCTGCTGTGGGCTGTGCTGCTGAGAGAAC 420

Qy 568 TTGGCCCAACTGCGGTGCTGGGATCTGAGCTCGGGCACAGAGTGGATCATCCAGGTG 627
Db 421 TTGGCCCAACTGCGGTGCTGGGATCTGAGCTCTGGGCACAGAGTGGATCATCCAGGTG 480

Qy 628 CCCATCTGGCATCTGTTGTGCTCAACTTCATCTCTTTTATCAACATCATCCGGGTGCTT 687
Db 481 CCCATCTGGCATCTGTTGTGCTCAACTTCATCTCTTTTATCAACATCATCCGGGTGCTT 540

Qy 688 GCCACTAAGCTTCGGGAGACCAATGCGGGCGGCTGTGACACCGAGGAGTACCG-GAA 746
Db 541 GCCACTAAGCTTCGGGAGACCAATGCGGGCGGCTGTGACACCGAGGAGTACCGGAGAA 600

Qy 747 GCTGCTCAGGTCCACGTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 804
Db 601 GCTGCTCAGGTCCACGTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

Qy 805 ATGGCTTGGCGGTACACCGAGGCTCTCAGGGACATTG-TGGCAGATCCAG-ATGCATTATG 862
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Qy 863 AG-ATGCTCTTCAACTCTCTCCAGGGATTTTGTGTCATCATA 906
Db 721 AGAATGCTCTTCAACTCTCTCCAGGGATTTGTTGTCATCATA 765
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Search completed: July 4, 2005, 02:48:48
Job time : 4780 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2005, 02:48:53 ; Search time 84 Seconds
(without alignments)
2002.866 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGARIAPSLALLCCPVLS.....EASGARPPPLQEGWETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2283	100.0	435	3 AAB07529	AAB07529 A mutant
2	2264.5	99.2	446	3 AAY96983	Aay96983 Tethered
3	2195	96.1	591	2 AAR92277	Aar92277 Rat bone
4	2195	96.1	591	2 AAW73316	Aaw73316 Parathyro
5	2195	96.1	591	8 ADH61247	Adh61247 Rat bone
6	2187	95.8	591	2 AAR27706	Aar27706 Rat bone
7	2187	95.8	591	7 ADE83416	Ade83416 Rat Prote
8	2146	94.0	591	8 ADO29629	Ado29629 Mouse GPC
9	2077.5	91.0	448	3 AAY96986	Aay96986 Human tet
10	2077.5	91.0	435	3 AAY96987	Aay96987 Human tet
11	2076.5	91.0	450	3 AAY96988	Aay96988 Human tet
12	2008	88.0	593	4 AAB71876	Aab71876 Human PTR
13	2008	88.0	593	6 ABP81872	Abp81872 Human par
14	2008	88.0	593	7 ADE83418	Ade83418 Human pro
15	2008	88.0	593	7 ADF70390	Adf70390 Human PTH
16	2008	88.0	593	8 ADO29628	Ado29628 Human GPC
17	2008	88.0	593	8 ADQ18189	Adq18189 Human sof
18	2008	88.0	593	8 ADQ76825	Adq76825 Human wil
19	2008	88.0	593	8 ADR47544	Adr47544 Human par
20	2002	87.7	593	2 AAW73317	Aaw73317 Human par
21	2002	87.7	593	4 ABB56385	Abb56385 Non-endog
22	2002	87.7	593	8 ADH61248	Adh61248 Human PTH
23	1960	85.9	593	2 AAR92278	Aar92278 Human kid
24	1957	85.7	595	6 ABG73825	Abg73825 Canine pa
25	1862.5	81.6	614	2 AAR27707	Aar27707 Human kid

26	1710	74.9	585	2 AAR27705	Aar27705 Opossum k
27	1710	74.9	585	2 AAR92276	Aar92276 Opossum k
28	1710	74.9	585	2 AAW73315	Aaw73315 Parathyro
29	1710	74.9	585	8 ADH61246	Adh61246 Opossum k
30	1698	74.4	964	7 ADC86169	Adc86169 Human GPC
31	1695	74.3	324	3 AAY96985	Aay96985 Tethered
32	1677.5	73.5	335	3 AAY96984	Aay96984 Tethered
33	1551	67.9	515	2 AAR92275	Aar92275 Opossum k
34	1551	67.9	515	2 AAW73314	Aaw73314 Parathyro
35	1551	67.9	515	8 ADH61245	Adh61245 Opossum k
36	1538	67.4	515	2 AAR27704	Aar27704 Opossum k
37	1478	64.7	975	8 ADQ76835	Adq76835 Parathyro
38	1465	64.2	536	3 AAY90230	Aay90230 Zebrafish
39	1465	64.2	536	3 AAY99600	Aay99600 Zebrafish
40	1465	64.2	536	7 ADC42305	Adc42305 Zebrafish
41	1465	64.2	536	7 ADH61059	Adh61059 Zebrafish
42	1151	50.4	542	3 AAY99601	Aay99601 Zebrafish
43	1130	49.5	542	7 ADC42307	Adc42307 Zebrafish
44	1130	49.5	542	7 ADH61061	Adh61061 Zebrafish
45	1122	49.1	523	3 AAY90231	Aay90231 Zebrafish

ALIGNMENTS

RESULT 1
AAB07529
ID AAB07529 standard; protein; 435 AA.

XX AAB07529;

AC AAB07529;

XX 20-OCT-2000 (first entry)

DT 20-OCT-2000 (first entry)

XX 20-OCT-2000 (first entry)

DE A mutant parathyroid hormone (PTH) receptor designated rdeltaNT.

XX A mutant parathyroid hormone (PTH) receptor designated rdeltaNT.

KW Mutant; parathyroid hormone; PTH; receptor; rdeltaNT;

XX Mutant; parathyroid hormone; PTH; receptor; rdeltaNT;

XX ligand binding domain.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

New parathyroid hormone (PTH) receptor, r-delta-NT, characterized by a deletion of the extracellular amino-terminus ligand binding domain, useful in screening assays for identifying agonists and antagonists of PTH receptor activity.

Claim 17; Fig 1; 81pp; English.

The present sequence represents a mutant parathyroid hormone (PTH) receptor, designated rdeltaNT. The polypeptide is characterised by a deletion of the extracellular amino-terminus ligand binding domain. The receptor has a minimal domain for ligand binding and is, therefore, useful in screening assays designed for the identification of agonists


```
CC and antagonists of PTH receptor activity
XX Sequence 435 AA;
SQ

Query Match 100.0%; Score 2283; DB 3; Length 435;
Best Local Similarity 100.0%; Pred. No. 4e-217;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGAARIAPSLALLCCPVLSSAYALVFDRIGMTYTVGYSMASLASLTAVLILAYFRRLH 60
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Qy 61 CTRNYIHHMFSLFMLRAASIFVKDAVLYSGFTLDEAERLTEERLHIIAQVPPPPAAA 120
Db 61 CTRNYIHHMFSLFMLRAASIFVKDAVLYSGFTLDEAERLTEERLHIIAQVPPPPAAA 120
Qy 121 GYACRVAVTFFLYFLATNYWILVEGLYLHSLIFMAFFSEKKYLGWFTIFGWLPAVF 180
Db 121 GYACRVAVTFFLYFLATNYWILVEGLYLHSLIFMAFFSEKKYLGWFTIFGWLPAVF 180
Qy 181 AVWGVRAATLANTCWDLSGGHKKWIIQVPIASVVLNFIIRVLAATKLRETNAGR 240
Db 181 AVWGVRAATLANTCWDLSGGHKKWIIQVPIASVVLNFIIRVLAATKLRETNAGR 240
Qy 241 CDTRQYRKLLRSLTLVLPFGVHYTVFMAIPYTEVSGTLWQIQMHYEMLPNSFGQFFVA 300
Db 241 CDTRQYRKLLRSLTLVLPFGVHYTVFMAIPYTEVSGTLWQIQMHYEMLPNSFGQFFVA 300
Qy 301 IIYFCNGEVOAEIRKSWRWTALDFKPKARSGSSSYSGPMVSHTSVTNVGPRAGLSL 360
Db 301 IIYFCNGEVOAEIRKSWRWTALDFKPKARSGSSSYSGPMVSHTSVTNVGPRAGLSL 360
Qy 361 PLSRPLPATTNGHSQIPGHAKPGAPATETETLPTVMAVPKDDGFLNGSCSGLDEEASGS 420
Db 361 PLSRPLPATTNGHSQIPGHAKPGAPATETETLPTVMAVPKDDGFLNGSCSGLDEEASGS 420
Qy 421 ARPPPLLOEGWETVM 435
Db 421 ARPPPLLOEGWETVM 435

RESULT 2
AA96983
ID AA96983 standard; protein; 446 AA.
XX AC AA96983;
XX DT 31-OCT-2000 (first entry)
XX DE Tethered PTH-1 receptor, Tether1.
XX KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
XX KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
XX OS Rattus sp.
XX OS Synthetic.
XX OS Chimeric.
XX FH Key
XX FH Peptide 1..23 Location/Qualifiers
FT /label= PTH-1_receptor_signal_sequence
FT Peptide 24..32
FT /label= PTH_residues_1-9
FT Peptide 33..36
FT /label= linker
FT Protein 37..446
FT /label= PTH-1_receptor
FT /note= "residue 182 to end"
XX WO200039278-A2.
XX PD 06-JUL-2000.
XX
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PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
DR N-PSDB; AAA51732.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 22; Fig 7; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)-n-B, R1-S-(L)-n-R or S-(L)-n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether activity, increasing CAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 446 AA;

Query Match 99.2%; Score 2264.5; DB 3; Length 446;
Best Local Similarity 97.3%; Pred. No. 2.8e-215;
Matches 434; Conservative 1; Mismatches 0; Indels 11; Gaps 1;

Qy 1 MGAARIAPSLALLCCPVLSSAYALVFDRIGMTYTVGYSMASLASLTVA 49
Db 1 MGAARIAPSLALLCCPVLSSAYALVFDRIGMTYTVGYSMASLASLTVA 60
Qy 50 VLIAYFRRLHCTRNTHHMFSLFMLRAASIFVKDAVLYSGFTLDEAERLTEERLHIIA 109
Db 61 VLIAYFRRLHCTRNTHHMFSLFMLRAASIFVKDAVLYSGFTLDEAERLTEERLHIIA 120
Qy 110 QVPPPPAAAAGVAGCRVAVTFFLYFLATNYWILVEGLYLHSLIFMAFFSEKKYLGWFT 169
Db 121 QVPPPPAAAAGVAGCRVAVTFFLYFLATNYWILVEGLYLHSLIFMAFFSEKKYLGWFT 180
Qy 170 IFGWGLPAVEVAVWVGVRATLANTGCDLSSGHKKWIIQVPIASVVLNFIIRVL 229
Db 181 IFGWGLPAVEVAVWVGVRATLANTGCDLSSGHKKWIIQVPIASVVLNFIIRVL 240
Qy 230 ATKLRNAGRCDTROQYRKLLRSLTLVLPFGVHYTVFMAIPYTEVSGTLWQIQMHYEM 289
Db 241 ATKLRNAGRCDTROQYRKLLRSLTLVLPFGVHYTVFMAIPYTEVSGTLWQIQMHYEM 300
Qy 290 LFNSFGQFFVAILIYFCNGEVOAEIRKSWRWTALDFKPKARSGSSSYSGPMVSHTSV 349
Db 301 LFNSFGQFFVAILIYFCNGEVOAEIRKSWRWTALDFKPKARSGSSSYSGPMVSHTSV 360
Qy 350 TNYGPRAGLSPLSPRLPATTNGHSQIPGHAKPGAPATETETLPTVMAVPKDDGFLNGS 409
Db 361 TNYGPRAGLSPLSPRLPATTNGHSQIPGHAKPGAPATETETLPTVMAVPKDDGFLNGS 420
Qy 410 CSGLDDEASGSARPPPLLOEGWETVM 435
Db 421 CSGLDDEASGSARPPPLLOEGWETVM 446
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XX PD 24-NOV-1998.
XX PF 06-JUN-1995; 95US-00471494.
XX PR 05-APR-1991; 91US-00681702.
XX PR 06-APR-1992; 92US-00864475.
XX PA (GEO) GEN HOSPITAL CORP.
XX PI Abou-Samra A, Juppner H, Potts JT, Segre GV, Schipani E;
XX PI Kronenberg HM;
XX XX WPI; 1999-034124/03.
XX DR N-PSDB; AAV08390.
XX XX Antibody to parathyroid hormone receptor - for diagnostic or therapeutic
XX PT use.
XX PS Claim 6; Fig 3; 63pp; English.
XX CC This sequence represents the rat parathyroid hormone (PTH) receptor R15B,
CC which is targeted by the antibody of the invention. The antibody of the
CC invention is immunoreactive with naturally occurring human, rat or
CC opossum PTH receptor. The antibody is useful for treating disorders
CC characterised by overstimulation of PTH receptors by their ligand and for
CC the diagnosis of PTH-related hypercalcaemia
XX SQ Sequence 591 AA;
Query Match 96.1%; Score 2195; DB 2; Length 591;
Best Local Similarity 73.6%; Pred. No. 3.2e-208;
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;
Qy 1 MGAARIAPSLALLCCFVLSAYAL----- 25
Db 1 MGAARIAPSLALLCCFVLSAYALVDADDVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA 60
Qy 26 ----- 25
Db 61 NIMESDKGWTASTSGKPKREKASGKFYPESKENKDVPTGSRRRGRPCLPEDWNIWCVPL 120
Qy 26 ----- 25
Db 121 GAGEVAVPCDPIYDFNKHGHAYRCDRNGSHEVVPGNRTWANYSECLKFWTNETRE 180
Qy 26 -EVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNIIHMHFSLPMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNIIHMHFSLPMLRAASIFVK 240
Qy 85 DAVLYSGFTLDEARLLEELHIIAQVPPPPAAAAGYACRVAVTFPLATNYWIL 144
Db 241 DAVLYSGFTLDEARLLEELHIIAQVPPPPAAAAGYACRVAVTFPLATNYWIL 300
Qy 145 VEGYLHSLIFMAPFSKKYLMGFTIFGWLPAVFVAVVGVVATLANTGCWDI-SSGHK 204
Db 301 VEGYLHSLIFMAPFSKKYLMGFTIFGWLPAVFVAVVGVVATLANTGCWDI-SSGHK 360
Qy 205 WIIQVPLASVNLFILFINIIRVLATKLRETNAGRCDTTQQYRKLLRSLTLVLPFGVH 264
Db 361 WIIQVPLASVNLFILFINIIRVLATKLRETNAGRCDTTQQYRKLLRSLTLVLPFGVH 420
Qy 265 YTVPMALPYTEVSTLWQIOMHYEMLFNSQGFVAILIYCFNGEVOAEIRKNSRWTLA 324
Db 421 YTVPMALPYTEVSTLWQIOMHYEMLFNSQGFVAILIYCFNGEVOAEIRKNSRWTLA 480
Qy 325 LDFRKARSSSSSYSGPMVSHSTVTNVGPRAGLSPLRPLPATTNGHSQLPGHAKPG 384
Db 481 LDFRKARSSSSSYSGPMVSHSTVTNVGPRAGLSPLRPLPATTNGHSQLPGHAKPG 540
Qy 385 APATETETLPVTMAVPKDDGFLNGSCSLDEASGSARPPPLIQEGWETVM 435
Db 541 APATETETLPVTMAVPKDDGFLNGSCSLDEASGSARPPPLIQEGWETVM 591

RESULT 5
ADH61247
ID ADH61247 standard; protein; 591 AA.
XX AC ADH61247;
XX DT 25-MAR-2004 (first entry)
XX XX Rat bone PTH/PTHrP receptor, R15B.
XX KW osteopathic; Parathyroid hormone receptor; hypercalcaemia;
XX KW hyperparathyroidism; osteoporosis; carcinoma; epidermoid cancer;
XX KW oesophagus multiple myeloma; hypocalcaemia; cytostatic; rat; PTH; PTHrP;
XX OS Rattus rattus.
XX PH Key Location/Qualifiers
FT Region 133..211
FT /note= "Transmembrane region 1"
FT Region 222..240
FT /note= "Transmembrane region 2"
FT Region 300..316
FT /note= "Transmembrane region 3"
FT Region 326..342
FT /note= "Transmembrane region 4"
FT Region 365..383
FT /note= "Transmembrane region 5"
FT Region 409..428
FT /note= "Transmembrane region 6"
FT Region 445..463
FT /note= "Transmembrane region 7"
XX US2003153041-A1.
XX PD 14-AUG-2003.
XX PF 09-OCT-2002; 2002US-00267730.
XX PR 05-APR-1991; 91US-00681702.
XX PR 06-APR-1992; 92US-00864475.
XX PR 06-JUN-1995; 95US-00471494.
XX PR 24-NOV-1998; 98US-00199874.
XX PA (GEO) GEN HOSPITAL CORP.
XX XX Segre GV, Kronenberg HM, Abou-Samra A, Juppner H, Potts JT;
XX PI Schipani E;
XX XX WPI; 2004-051107/05.
XX DR N-PSDB; ADH61258.
XX PT New isolated DNA encoding parathyroid hormone receptor polypeptides,
XX PT useful for diagnosing and treating disorders associated with parathyroid
XX PT hormone receptors, e.g. hypercalcaemia, osteoporosis or multiple myeloma.
XX PS Disclosure; SEQ ID NO 20; 71pp; English.
XX CC The invention relates to parathyroid hormone (PTH) receptor and its
XX CC corresponding nucleic acid sequence. The parathyroid hormone receptor
XX CC polypeptides, polynucleotides and antibodies are useful for diagnosing,
XX CC prognosticating and treating disorders associated with parathyroid
XX CC hormone receptors, e.g. hypercalcaemia, hyperparathyroidism,
XX CC osteoporosis, carcinomas of the breast, lung and prostate, epidermoid
XX CC cancers of the head and neck of the oesophagus, multiple myeloma, or
XX CC hypocalcaemia. The DNAs and polypeptides are also useful for screening
XX CC candidate compounds for antagonistic or agonistic effects on parathyroid
XX CC hormone receptor activity. The compounds are also useful in manufacturing
XX CC diagnostic agents used as diagnostic tools to diagnose hypercalcaemia and
XX CC to distinguish between hypercalcaemic conditions. The present sequence is
XX CC rat bone PTH/PTHrP (PTH-related protein) receptor protein.

541 APATETETLPVTMAVPKDDGLNGSCSGLDEASGSARPPPLLOEGWETM 591

Matches 434; Conservative 0; Mismatches 1; Indels 156; Gaps 1;

QY 1 MGAARTAPSIALLCCPVLSAVAL----- 25
DB 1 MGAARTAPSIALLCCPVLSAVALDDVFTKEQIFLLHRAQAQCKLLKEVLHTAA 60
QY 26 ----- 25
DB 61 NIMESDKGWTTPASTSGKPRKEKASGFYPESKENKDVPDTSRRRGRPCLPEDWNIWCWPL 120
QY 26 ----- 25
DB 121 GAPGEVAVVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPVGNRTWANYSECLKFTMTNRE 180
QY 26 -EVFDRLGMIYTVGYSMASLTVAVLIILAYFRLHCTRNVIHMHMFLSFMRAASIFVK 84
DB 181 REVFDRLGMIYTVGYSMASLTVAVLIILAYFRLHCTRNVIHMHMFLSFMRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLITEBELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYLATNYYWIL 144
DB 241 DAVLYSGFTLDEAERLITEBELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYLATNYYWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLPAVFAVWVGVVAVTATLANTGCDLSSGHKK 204
DB 301 VEGLYLHSLIFMAFFSEKKYLGFTIFGWLPAVFAVWVGVVAVTATLANTGCDLSSGHKK 360
QY 205 WIIQVPILASVVLNFIINIRVLATKLRETNAGRCTRQYRKLLRSLVLVPLFGVH 264
DB 361 WIIQVPILASVVLNFIINIRVLATKLRETNAGRCTRQYRKLLRSLVLVPLFGVH 420
QY 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFVAIIYFCNGEVOAERKSWSRWTLA 324
DB 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFQGFVAIIYFCNGEVOAERKSWSRWTLA 480
QY 325 LDFKRVARGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRPATNGHSQLPGHAKPG 384
DB 481 LDFKRVARGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRPATNGHSQLPGHAKPG 540
QY 385 APATETETLPVTMAVPKDDGLNGSCSGLDEASGSARPPPLLOEGWETM 435
DB 541 APATETETLPVTMAVPKDDGLNGSCSGLDEASGSARPPPLLOEGWETM 591

RESULT 8
ADO29629
ID ADO29629 standard; protein; 591 AA.
XX ADO29629;
AC ADO29629;
DT 29-JUL-2004 (first entry)
DE Mouse GPCR PTHR1, SEQ ID NO:731.
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
XX transgenic mouse; neurological disorder; adrenal gland disorder;
XX colon disorder; intestinal disorder; cardiovascular disorder;
XX muscular disorder; blood disorder; immune disorder; bone disorder;
XX joint disorder; metabolic disorder; nutritive disorder; cancer;
XX kidney disorder; liver disorder; lung disorder; breast disorder;
XX ovary disorder; uterus disorder; prostate disorder; testis disorder;
XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;
XX thymus disorder; thyroid disorder; antiparkinsonian; antitumor;
XX cytostatic; antiinflammatory; vasotropic; antidiarrhoeal; antidiabetic;
XX CNS; central nervous system; respiratory; antidiarrhoeal; antidiabetic;
XX virucide; hepatocytotoxic; antibacterial; antianemic; antiseborrheic;
XX dermatological; antitumor; antithyroid; antiallergic; anorectic;
XX immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
XX murine; receptor.
OS Mus musculus.
XX
XX W02004040000-A2.
XX

Db ADE83416
ID ADE83416 standard; protein; 591 AA.
XX ADE83416;
AC ADE83416;
DT 29-JAN-2004 (first entry)
XX Rat Protein P25961, SEQ ID NO 11011.
DE
DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
KW Rattus norvegicus.
OS
XX W02003016475-A2.
PN
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI WPI; 2003-268312/26.
XX GENBANK; P25961.
DR
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC Claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
CC injury (CCI) and spared nerve injury (SNI)).
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 591 AA;
SQ

Query Match 95.8%; Score 2187; DB 7; Length 591;
Best Local Similarity 73.4%; Pred. No. 2e-207;

PD 13-MAY-2004.
XX 09-SEP-2003; 2003WO-US028226.
XX 09-SEP-2002; 2002US-0409303P.
XX 09-APR-2003; 2003US-0461329P.
XX (PRIM-) PRIMAL INC.
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX WPI; 2004-390329/36.
DR N-PSDB; ADO30323.
XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX Claim 151; SEQ ID NO 731; 542pp; English.
XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCR) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 591 AA;
Query Match 94.0%; Score 2146; DB 8; Length 591;
Best Local Similarity 72.1%; Pred. No. 2.3e-203;
Matches 426; Conservative 2; Mismatches 7; Indels 156; Gaps 1;
QY 1 MGAARIAPSLALLCCPVLSSAYAL-----25
DB 1 MGTARIAPSLALLCCPVLSSAYALVDADVFTEKEQIFLLHRAQCDKLLKEVLHTAA 60
QY 26 -----25
DB 61 NIMESDKGMTASTSGKPRKEKAPGKFPYPSKENKOVPTGSRRRGRPCLPEDWNVCWPL 120
QY 26 -----25
DB 121 GAGEVVAVPCDDIYDFNHKHAIRYRCDRNGSEVVPGNRTWANYSECLKFWMTRE 180
QY 26 -EVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRYNIHMFSLPMLRAASIFVK 84

DB 181 REVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRYNIHMFSLPMLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTBEELHIIAQVPPPPAAAAGYACRVAVTFFLYFLATNYWIL 144
DB 241 DAVLYSGFTLDEAERLTBEELHIIAQVPPPPAAAAGYACRVAVTFFLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGMGLPAVFVAVVGVVVRATLANTCWDLSGHHK 204
DB 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGMGLPAVFVAVVGVVVRATLANTCWDLSGHHK 360
QY 205 WIIQVPIIASVNLNFIINIRVATKLRBTNAGRCDTROQYRKLRLSLVLVPLFGVH 264
DB 361 WIIQVPIIASVNLNFIINIRVATKLRBTNAGRCDTROQYRKLRLSLVLVPLFGVH 420
QY 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFVAVIIFCFCNGEVOAERKSWRWTLA 324
DB 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFVAVIIFCFCNGEVOAERKSWRWTLA 480
QY 325 LDFKRRKARGSSSYSGPMVSHSTVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPG 384
DB 481 LDFKRRKARGSSSYSGPMGHAHTSVTVNGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPG 540
QY 385 APATETETPLVTMAYPKDDGFLNGSCSGLDEEASGARPPPLLOEGWETVM 435
DB 541 APAIENETIPVTMTVPKDDGFLNGSCSGLDEEASGARPPPLLOEGWETVM 591
RESULT 9
AA996986
ID AA996986 standard; protein; 448 AA.
XX AC
XX AA996986;
DT 31-OCT-2000 (first entry)
XX Human tethered PTH-1 receptor, Tether1.
DE PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.
XX Homo sapiens.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
FT Peptide 1..23
FT /label= Signal sequence
FT /note= "Human PTH-1 receptor residues 1-23"
FT Peptide 24..32
FT /label= PTH(1-9)
FT Peptide 33..36
FT /label= Linker
FT Protein 37..448
FT /label= PTH-1 receptor
FT /note= "Human PTH-1 receptor residues 182-593"
XX WO200039278-A2.
PN 06-JUL-2000.
XX 30-DEC-1999; 99WO-US031108.
PR 31-DEC-1998; 98US-0114577P.
XX (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
PI WPI; 2000-452384/39.
DR

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DR N-PSDB; AAA51735.
XX
XX New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
XX Example 4; Fig 17; 119pp; English.
XX
XX Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether activity, increasing CAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
XX Sequence 448 AA;
SQ
Query Match 91.0%; Score 2077.5; DB 3; Length 448;
Best Local Similarity 88.8%; Pred. No. 9.8e-197;
Matches 398; Conservative 11; Mismatches 26; Indels 13; Gaps 3;
QY 1 MGAARIAPSLALLCCPVLSSAYAL-----EVFDRLGMIYTVGYSMASLITVA 49
DB 1 MGTARIAPGLALLCCPVLSSAYAVSEIQLMHGGGGEVFDRLGMIYTVGYSVSLITVA 60
QY 50 VLILAYPRRLHCTRNYYHMFSLFMLRAASIFVKDVLVYSGFTLDEAERLTDEELHIIA 109
DB 61 VLILAYPRRLHCTRNYYHMFSLFMLRAVSIKVDVLVYSGATLDEAERLTDEELRAIA 120
QY 110 QVPPPPAAAGVAGCVAVTFEFLYFLATNYMILVEGLYHSLIFMAFFSEKKYLWGFT 169
DB 121 QAPPPPPATAAGVAGCVAVTFEFLYFLATNYMILVEGLYHSLIFMAFFSEKKYLWGFT 180
QY 170 IFWGLPAVFAVAVVGVVVRATLANTGCDLSSGHKKWIIQVPIIASVVLNFIINIRVL 229
DB 181 VFGWGLPAVFAVAVVVRATLANTGCDLSSGNKKWIIQVPIIASIVLNFILINIRVL 240
QY 230 ATKLRNAGCDTROQYRKLLRSTLVLPLFGVHYTVFMAFPYTEVSGTLQIQMHYEM 289
DB 241 ATKLRNAGCDTROQYRKLLRSTLVLMLPLFGVHYTVFMAFPYTEVSGTLQIQMHYEM 300
QY 290 LFNSFQGFVVAIIYFCNGEVOAEIRKSWSRWTLALDFKFKARSGSSSYSGPMVSHTSV 349
DB 301 LFNSFQGFVVAIIYFCNGEVOAEIRKSWSRWTLALDFKFKARSGSSSYSGPMVSHTSV 360
QY 350 TNGVPRAGLSPLSPR-LPPATTNGHSQLPGHAKPGAPATET-ETLPVTMAVPRKDDGFLN 407
DB 361 TNGVPRVGLPLSPRLPATTNGHSQLPGHAKPGTPALETETTPPMAAPKDDGFLN 420
QY 408 GSCSGLDEEASGARPPPLLOEGHETVM 435
DB 421 GSCSGLDEEASGARPPPALLOEHWETVM 448
RESULT 10
AA96987
ID AA96987 standard; protein; 435 AA.
XX
XX AC AA96987;
XX
XX DT 31-OCT-2000 (first entry)
XX
XX DE Human tethered PTH-1 receptor, hdelNT.
XX
XX KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;

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KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
XX
XX Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
XX WO200039278-A2.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US031108.
XX
XX 31-DEC-1998; 98US-0114577P.
XX
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
XX DR N-PSDB; AAA51736.
XX
XX New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
XX Example 4; Fig 18; 119pp; English.
XX
XX Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether activity, increasing CAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
XX Sequence 435 AA;
SQ
Query Match 91.0%; Score 2077; DB 3; Length 435;
Best Local Similarity 90.8%; Pred. No. 1.1e-196;
Matches 397; Conservative 10; Mismatches 26; Indels 4; Gaps 3;
QY 1 MGAARIAPSLALLCCPVLSSAYALVFDRGLMIYTVGYSMASLITVAIILAYPRRLH 60
DB 1 MGTARIAPGLALLCCPVLSSAY--EVFDRLGMIYTVGYSVSLITVAIILAYPRRLH 58
QY 61 CTENYIHMELFSLFMLRAASIFVKDVLVYSGFTLDEAERLTDEELHIIAQVPPPPAAAV 120
DB 59 CTENYIHMELFSLFMLRAVSIKVDVLVYSGATLDEAERLTDEELRAIAQAPPPATAA 118
QY 121 GYACRCVAVTFEFLYFLATNYMILVEGLYHSLIFMAFFSEKKYLWGFTIFGWLPAV 180
DB 119 GYACRCVAVTFEFLYFLATNYMILVEGLYHSLIFMAFFSEKKYLWGFTVFGWGLPAV 178
QY 181 AVWGVVRATLANTGCDLSSGHKKWIIQVPIIASVVLNFIINIRVLATKLRETNAGR 240
DB 179 AVWGVVRATLANTGCDLSSGNKKWIIQVPIIASIVLNFILINIRVLATKLRETNAGR 238
QY 241 CDTRQOYRKLLRSTLVLPLFGVHYTVFMAFPYTEVSGTLQIQMHYEMLFNSFQGFVVA 300
DB 239 CDTRQOYRKLLRSTLVLMLPLFGVHYTVFMAFPYTEVSGTLQIQMHYEMLFNSFQGFVVA 298
QY 301 ILYCFNGEVOAEIRKSWSRWTLALDFKFKARSGSSSYSGPMVSHTSVTNVPGRAGLSL 360

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Db      299 ILYCFNGEVOAEIKWSRWTLALDFKRSKSSSYSGPMVSHSTVTNNGPRVGLGL 359
Qy      361 PLSPR-LPPATNGHSQLPGHAKPGAPATET-ETLPVTMAVPKDDGLNGSCGLDEAS 418
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      359 PLSRLLPTATNGHPQLPGHAKPGTPALETLETPPAMAAPKDDGLNGSCGLDEAS 418
Qy      419 GSARPPPLLOEGWETVM 435
      | ||| ||||| |||||
Db      419 GPERPPALLOEWETVM 435

RESULT 11
AAY96988
ID      AAY96988 standard; protein; 450 AA.
XX
AC      AAY96988;
XX
DT      31-OCT-2000 (first entry)
XX
DE      Human tethered PTH-1 receptor, Tether-R11.
XX
KW      PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW      PTH-1 receptor; resorption; remodeling; tether-R11; osteoporosis; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
OS      Chimeric.
XX
Key      Location/Qualifiers
Peptide  1..23
          /label= Signal sequence
          /note= "Human PTH-1 receptor residues 1-23"
Peptide  24..34
          /label= PTH(1-11)
Peptide  35..38
          /label= Linker
Protein  39..450
          /label= PTH-1 receptor
          /note= "Human PTH-1 receptor residues 182-593"
XX
W0200039278-A2.
XX
06-JUL-2000.
XX
30-DEC-1999; 99WO-US031108.
XX
31-DEC-1998; 98US-0114577P.
XX
(GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
WPI; 2000-452384/39.
DR N-PSDB; AAA51737.
XX
New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
Example 4; Fig 19; 119pp; English.
XX
Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n
-R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases

```

```

CC and disorders associated with decreased tether1 activity, increasing CAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrp which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ      Sequence 450 AA;
      Query Match      91.0%; Score 2076.5; DB 3; Length 450;
      Best Local Similarity 88.4%; Pred. No. 1.2e-196;
      Matches 398; Conservative 11; Mismatches 26; Indels 15; Gaps 3;

Qy      1 MGAARIAPSLALLCCPVLSAYAL-----EVDRLGMIYTYGYSMASLASLT 47
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MGTARIAPGLALLCCPVLSAYAVSEIQLMHNRRGGGEVDFRLGMIYTYGYSVSLASLT 60
Qy      48 VAVLILAYFRRLHCTRNHYHMHMFLSFMLRAASIFVKDAVLYSGFTLDEABRLTEELHI 107
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 VAVLILAYFRRLHCTRNHYHMHFLSFMLRAVSI FVKDAVLYSGATLDEABRLTEELRA 120
Qy      108 IAQVPPPPAAAAGYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLMG 167
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 IAQAPPPPPATAAGYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLMG 180
Qy      168 FTIFGWLPAVFAVWVWVRATLANTGCDLSSGHKKWIIQVPILASVVLNFIPIINIR 227
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      181 FTVFGWGLPAVFAVWVWVRATLANTGCDLSSGNKKWIIQVPILASIVLNFILFINIVR 240
Qy      228 VLATKLRETNAGRCDTROQYRKLRLSTLVLVPLFGVHYTVFMALPYTEVSGTLWQIMHY 287
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      241 VLATKLRETNAGRCDTROQYRKLRLSTLVLVPLFGVHYTVFMALPYTEVSGTLWQIMHY 300
Qy      288 EMLFNSFQGFVVAIIYFCNGEVOAEIRKSWRWTALDFFKRSKSSSYSGPMVSHST 347
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      301 EMLFNSFQGFVVAIIYFCNGEVOAEIRKSWRWTALDFFKRSKSSSYSGPMVSHST 360
Qy      348 SVTNVGPRAGLSLPLSPR-LPPATNGHSQLPGHAKPGAPATET-ETLPVTMAVPKDDGF 405
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      361 SVTNVGPVGLGLPLSPRLPTATTNGHPOLPGHAKPGTPALETLETPPAMAAPKDDGF 420
Qy      406 LKNGCSGLDEASGSARPPPLLOEGWETVM 435
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      421 LKNGCSGLDEASGPERPPALLOEWETVM 450

RESULT 12
AAB71876
ID      AAB71876 standard; protein; 593 AA.
XX
AC      AAB71876;
XX
DT      03-MAY-2001 (first entry)
XX
DE      Human PTHR seven transmembrane domain.
XX
KW      Human; parathyroid hormone/parathyroid hormone-related peptide receptor;
KW      PTHR; h15571; immunomodulatory; vascular; hepatic; antidiasthma;
KW      antimicrobial; antiinflammatory; immunosuppressive; gene therapy;
KW      vaccine; G-protein coupled receptor; GPCR; liver fibrosis;
KW      respiratory disorder; infection; chronic inflammatory disease;
KW      organ-specific autoimmunity; graft rejection; cystic fibrosis.
XX
OS      Homo sapiens.
XX
PN      W0200109328-A1.
XX
PD      08-FEB-2001.
XX
PF      03-AUG-2000; 2000WO-US021278.
XX
PR      03-AUG-1999; 99US-0146916P.
XX      29-FEB-2000; 2000US-00515781.
XX

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PA (MILL-) MILLENNIUM PHARM INC.
XX Hodge MR, Lloyd C, Weich NS;
XX WPI; 2001-138653/14.
PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma.
XX Disclosure; Fig 2; 145pp; English.
PS
XX The present sequence is a human G-protein coupled receptor (GPCR) used
CC for comparison with the seven transmembrane domain of a novel GPCR
CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate GPCR expression. Such diseases includes immune,
CC haematological, fibrotic, hepatic and respiratory disorders including
CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
CC graft rejection, graft versus host disease, cystic fibrosis and, in
CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
CC in the production of antibodies against GPCR and in assays to identify
CC modulators (agonists and antagonists) of GPCR expression and activity.
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
CC used as diagnostic agents for detecting the presence of GPCR polypeptides
CC in samples
XX
SQ Sequence 593 AA;
Query Match 88.0%; Score 2008; DB 4; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.1e-189;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;
Qy 1 MGAARTAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADVTWKEQIFULHRAQAQCEKRLKEVLQRP 60
Qy 26 ----- 25
Db 61 SIMESDKGWTSASTGKPRKDKASGLYPESEEDKEAPTGSRYGRPCLPEDWHLCWPL 120
Qy 26 ----- 25
Db 121 GAGEVAVPCPDYIDFNHKGHAYRCRDNGSWELVPGHNRWTANYSECVKELTNETRE 180
Qy 26 -EVFDRLGMIYTVGYSMASLTAVLILAYFRRLHCTRNYIHMHFSLFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASTVAVLILAYFRRLHCTRNYIHMHFSLFMLRAVSIFVK 240
Qy 85 DAVLYSGFTLDEARLTERELHIIAQVPPPPAAAAGYACRVAVTFFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEARLTERELRAIAQAPPPPPATAAAGYACRVAVTFFLYFLATNYWIL 300
Qy 145 VEGLYLSHLIFMAPFSEKKYLWGFTIFGWGLPAFVAVVWGVVRATLANTGCWDLSSGHKK 204
Db 301 VEGLYLSHLIFMAPFSEKKYLWGFTIFGWGLPAFVAVVWGVVRATLANTGCWDLSSGNKK 360
Qy 205 WIIQVPLASVLNFIILFIIIRVLATKLRETNAGRCDTTQQYRKLLRLSTLVLPFGVH 264
Db 361 WIIQVPLASVLNFIILFIIIRVLATKLRETNAGRCDTTQQYRKLLKSTLVLMPLFGVH 420
Qy 265 YTVFMAPLYTEVSTLWQIQHYEMLFNSQGFVVAIYFCNGEVAQAEIKKSWRWTLA 324
Db 421 YIVFMATPYTEVSTLWQVQHYEMLFNSQGFVVAIYFCNGEVAQAEIKKSWRWTLA 480
Qy 325 LDFRKARSSSSYSYSGPMWSTHTSVTVNGVRAGLSPLSPR-LPPATTNGHSGOLPGHAKP 383
Db 481 LDFRKARSSSSYSYSGPMWSTHTSVTVNGVRAGLSPLSPRLLPATTNGHSGOLPGHAKP 540
Qy 384 GAPATET-ETLPVTMAYPKDDGFLNGSCSLGDEEASGARPPPLPQEWETVM 435
Db 541 GTPALETLETTTPPAAAPKDDGFLNGSCSLGDEEASGARPPPALPQEWETVM 593

RESULT 13
ABP81872
ID ABP81872 standard; protein; 593 AA.
XX
AC ABP81872;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human parathyroid hormone receptor 1 protein SEQ ID NO:229.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
OS Homo sapiens.
XX
PN WQ200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
DR N-PSDB; AB242719.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

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OM protein - protein search, using sw model

Run on: July 4, 2005, 05:24:16 ; Search time 27 Seconds
(without alignments)
1202.679 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGSARPPPLQEGWETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2195	96.1	591	2	US-08-468-249A-20
2	2008	88.0	593	4	US-09-631-603-21
3	2002	87.7	593	2	US-08-468-249A-21
4	2002	87.7	593	4	US-09-826-509-563
5	1710	74.9	595	1	US-08-142-439A-6
6	1710	74.9	585	2	US-08-142-551B-125
7	1710	74.9	585	2	US-08-869-477-6
8	1710	74.9	585	2	US-08-468-249A-19
9	1551	67.9	535	2	US-08-468-249A-18
10	1465	64.2	536	4	US-09-449-632-2
11	1130	49.5	542	4	US-09-449-632-4
12	1068	46.8	575	4	US-09-449-632-5
13	1050.5	46.0	550	4	US-09-631-603-20
14	1044.5	45.8	550	4	US-09-826-509-565
15	1036	45.4	541	3	US-08-468-011A-2
16	1036	45.4	541	3	US-09-236-468A-2
17	1036	45.4	541	5	PCT-US95-07085-2
18	960.5	42.1	207	4	US-08-811-519-31
19	776	34.0	459	4	US-09-694-519-4
20	775.5	34.0	1324	2	US-08-811-897A-56
21	775.5	34.0	1324	3	US-09-201-474-56
22	773.5	33.9	444	4	US-09-694-519-6
23	772	33.8	459	4	US-09-694-519-3
24	772	33.8	459	4	US-09-694-519-8
25	762.5	33.4	458	1	US-08-112-817C-2
26	762.5	33.4	458	4	US-09-694-519-5
27	762.5	33.4	458	4	US-09-694-519-7

28	757.5	33.2	449	1	US-08-142-439A-5
29	757.5	33.2	449	2	US-08-869-477-5
30	752.5	33.0	457	4	US-09-631-603-23
31	752.5	33.0	457	4	US-09-694-519-1
32	747	32.7	440	4	US-09-631-603-22
33	746.5	32.7	457	4	US-09-826-509-579
34	741	32.5	460	4	US-09-694-519-2
35	738	32.3	440	4	US-09-826-509-567
36	718	31.4	447	4	US-09-694-519-9
37	687	30.1	448	2	US-08-811-897A-22
38	687	30.1	448	3	US-08-855-213-22
39	687	30.1	448	3	US-09-201-474-22
40	687	30.1	468	4	US-09-631-603-19
41	687	30.1	525	2	US-08-811-897A-23
42	687	30.1	525	2	US-08-855-213-23
43	687	30.1	525	3	US-09-201-474-23
44	684	30.0	448	2	US-08-811-897A-18
45	684	30.0	448	2	US-08-855-213-18

ALIGNMENTS

RESULT 1
US-08-468-249A-20
; Sequence 20, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-249A-20

Query Match 96.1%; Score 2195; DB 2; Length 591;
Best Local Similarity 73.6%; Pred. No. 1e-209;
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;

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QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGAARIAPSLALLCCPVLSSAYALVDADDVFTKEBQIFLLHRAQAQCDKLLKEVLHTAA 60
QY 26 ----- 25
Db 61 NIMESDKGWTASTSGKPRKEKAGKFPESKENKDVPTGSRRRGRPCLPEDWNICWPL 120
QY 26 ----- 25
Db 121 GAPGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRWTANYSECVKFLTNRE 180
QY 26 ----- 25
Db 26 -EVFDRGLMIYTVGYSMASLASLTAVLILAYFRRLHCTRNYIHMHPLSFMLRAASIFVK 84
181 REVFDRLGMIYTVGYSMASLASLTAVLILAYFRRLHCTRNYIHMHPLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTEBELHIIAQVPPPPAAAAGYAGCRVAVTFPLYFLATNYWIL 144
241 DAVLYSGFTLDEAERLTEBELHIIAQVPPPPAAAAGYAGCRVAVTFPLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLGWFTIFGWLGPDAVFVAVVWVGVVRATLANTGCWDLSSGHKK 204
301 VEGLYLHSLIFMAFFSEKKYLGWFTIFGWLGPDAVFVAVVWVGVVRATLANTGCWDLSSGHKK 360
QY 205 WIIQVPIASVLNFIILFINIRVLATKURETNAGRCDTROQYRKLLRSTLVLPVLFVGH 264
361 WIIQVPIASVLNFIILFINIRVLATKURETNAGRCDTROQYRKLLRSTLVLPVLFVGH 420
QY 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWRWTLA 324
421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWRWTLA 480
QY 325 LDFPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPG 384
481 LDFPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKPG 540
QY 385 APATETETLPTVMAVPKDDGFLNGSCGLDEASGSRPPLLOEGWETVM 435
541 APATETETLPTVMAVPKDDGFLNGSCGLDEASGSRPPLLOEGWETVM 591
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RESULT 2

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US-09-631-603-21
; Sequence 21, Application US/09631603
; Patent No. 6733990
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Lloyd, Clare
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: 15571, A No. 6733990el GPCR-like Molecule of the
; FILE REFERENCE: 5800-48A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US/09/631.603
; PRIOR FILING DATE: 2000-08-03
; PRIOR FILING DATE: 2000-02-29
; PRIOR FILING DATE: 2000-04-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-631-603-21
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Query Match 88.08; Score 2008; DB 4; Length 593;
Best Local Similarity 67.38; Pred. No. 4.3e-191;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEBQIFLLHRAQAQCEKRLKEVLQRP 60
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QY 26 ----- 25
Db 61 SIMESDKGWTASTSGKPRKDKASGKLYPESEBEDKEAPTGSRYRGRPCLPEDWHILCWPL 120
QY 26 ----- 25
Db 121 GAPGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRWTANYSECVKFLTNRE 180
QY 26 -EVFDRGLMIYTVGYSMASLASLTAVLILAYFRRLHCTRNYIHMHPLSFMLRAASIFVK 84
181 REVFDRLGMIYTVGYSMASLASLTAVLILAYFRRLHCTRNYIHMHPLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTEBELHIIAQVPPPPAAAAGYAGCRVAVTFPLYFLATNYWIL 144
241 DAVLYSGFTLDEAERLTEBELHIIAQVPPPPAAAAGYAGCRVAVTFPLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLGWFTIFGWLGPDAVFVAVVWVGVVRATLANTGCWDLSSGHKK 204
301 VEGLYLHSLIFMAFFSEKKYLGWFTIFGWLGPDAVFVAVVWVGVVRATLANTGCWDLSSGHKK 360
QY 205 WIIQVPIASVLNFIILFINIRVLATKURETNAGRCDTROQYRKLLRSTLVLPVLFVGH 264
361 WIIQVPIASVLNFIILFINIRVLATKURETNAGRCDTROQYRKLLRSTLVLPVLFVGH 420
QY 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWRWTLA 324
421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWRWTLA 480
QY 325 LDFPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKP 383
481 LDFPKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQLPGHAKP 540
QY 384 GAPATTT-ETFLPVTMAVPKDDGFLNGSCGLDEASGSRPPLLOEGWETVM 435
541 GTPALETETLPTVMAVPKDDGFLNGSCGLDEASGSRPPLLOEGWETVM 593

RESULT 3
US-08-468-249A-21
; Sequence 21, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
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TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-21

Query Match 87.7%; Score 2002; DB 2; Length 593;
Best Local Similarity 67.1%; Pred. No. 1.7e-190;
Matches 398; Conservative 10; Mismatches 27; Indels 158; Gaps 3;
QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
DB 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLORPA 60
QY 26 ----- 25
DB 61 SIMESDKGWTASSTGKPKDKASGLYPSEEDKEAPTGSRYGRPCLPEDWDHILCWPL 120
QY 26 ----- 25
DB 121 GAGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRWTWANYSECVKFLTNRE 180
QY 26 -EYFDRGLGMIYTYGYSMSLASLTAVLILAYFRRLHCTRYNIHMHMFLSPMLRAASIFVK 84
DB 181 REVFDRLGMIYTYGYSVSLASLTAVLILAYFRRLHCTRYNIHMHMFLSPMLRAVSIFVK 240
QY 85 DAVLYSGFTLDEARLLEEELHIIAQVPPPPAAAGYACRVAVTFPLFLATNYTWIL 144
DB 241 DAVLYSGATLDEARLLEEELRAIAQAPPPATAAGYACRVAVTFPLFLATNYTWIL 300
QY 145 VEGLYLHSLIFMAFPSEKKYLWGTFIFGWGLPAVFVAVVWVGVVRATLANTCGWDLSSGHKK 204
DB 301 VEGLYLHSLIFMAFPSEKKYLWGTFVFGWGLPAVFVAVVWVSVRATLANTCGWDLSSGNKK 360
QY 205 WIQVPIASVNLNFIINIRVLATKLRBTNAGRCDTTQQYRKLRLSTLVLVPLFGVH 264
DB 361 WIQVPIASVNLNFIINIRVLATKLRBTNAGRCDTTQQYRKLKLSLVLVPLFGVH 420
QY 265 YTVFMAPYTEVSGTLQVQHYEMLFNSFGQFFVAILIYFCNGEVOAEIKKSWSRWTLA 324
DB 421 YIVFMAPYTEVSGTLQVQHYEMLFNSFGQFFVAILIYFCNGEVOAEIKKSWSRWTLA 480
QY 325 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383
DB 481 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLPTATTNGHPQLPGHAKP 540
QY 384 GAPATET-ETLPTVMTAVPKDDGFLNGSCSGLDEASGSARPPPLLOEGWETVM 435
DB 541 GTPALETLETPPAMAAPKDDGFLNGSCSGLDEASGPERPPALLQBEWETVM 593

RESULT 4

US-09-826-509-563
; Sequence 563, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826.509
; CURRENT FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-563

Query Match 87.7%; Score 2002; DB 4; Length 593;
Best Local Similarity 67.1%; Pred. No. 1.7e-190;
Matches 398; Conservative 10; Mismatches 27; Indels 158; Gaps 3;
QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
DB 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLORPA 60
QY 26 ----- 25
DB 61 SIMESDKGWTASSTGKPKDKASGLYPSEEDKEAPTGSRYGRPCLPEDWDHILCWPL 120
QY 26 ----- 25
DB 121 GAGEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWELVPGHNRWTWANYSECVKFLTNRE 180
QY 26 -EYFDRGLGMIYTYGYSMSLASLTAVLILAYFRRLHCTRYNIHMHMFLSPMLRAASIFVK 84
DB 181 REVFDRLGMIYTYGYSVSLASLTAVLILAYFRRLHCTRYNIHMHMFLSPMLRAVSIFVK 240
QY 85 DAVLYSGFTLDEARLLEEELHIIAQVPPPPAAAGYACRVAVTFPLFLATNYTWIL 144
DB 241 DAVLYSGATLDEARLLEEELRAIAQAPPPATAAGYACRVAVTFPLFLATNYTWIL 300
QY 145 VEGLYLHSLIFMAFPSEKKYLWGTFIFGWGLPAVFVAVVWVGVVRATLANTCGWDLSSGHKK 204
DB 301 VEGLYLHSLIFMAFPSEKKYLWGTFVFGWGLPAVFVAVVWVSVRATLANTCGWDLSSGNKK 360
QY 205 WIQVPIASVNLNFIINIRVLATKLRBTNAGRCDTTQQYRKLRLSTLVLVPLFGVH 264
DB 361 WIQVPIASVNLNFIINIRVLATKLRBTNAGRCDTTQQYRKLKLSLVLVPLFGVH 420
QY 265 YTVFMAPYTEVSGTLQVQHYEMLFNSFGQFFVAILIYFCNGEVOAEIKKSWSRWTLA 324
DB 421 YIVFMAPYTEVSGTLQVQHYEMLFNSFGQFFVAILIYFCNGEVOAEIKKSWSRWTLA 480
QY 325 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383
DB 481 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLPTATTNGHPQLPGHAKP 540
QY 384 GAPATET-ETLPTVMTAVPKDDGFLNGSCSGLDEASGSARPPPLLOEGWETVM 435
DB 541 GTPALETLETPPAMAAPKDDGFLNGSCSGLDEASGPERPPALLQBEWETVM 593

RESULT 5

US-08-142-439A-6
; Sequence 6, Application US/08142439A
; Patent No. 5670360
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5670360 No. 5670360disk of No. 5670360th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/142,439A
APPLICATION NUMBER: 24-NOV-93
FILING DATE: 24-NOV-93
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-MAR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3756.204-US
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Didelphis virginiana
US-08-142-439A-6

Query Match 74.9%; Score 1710; DB 1; Length 585;
Best Local Similarity 80.2%; Pred. No. 2e-161;
Matches 333; Conservative 27; Mismatches 42; Indels 13; Gaps 7;
QY 26 EVFDRGLMIYTVGYSMASLTAVLILAYFRRLHCTRNVIHMHMFLSFMLRAASIFVKD 85
DB 179 EVFDRGLMIYTVGYSLGSLTAVLILGYFRRLHCTRNVIHMHMFLSFMLRAVSIFIKD 238
QY 86 AVLYSGTDLDEARLTFEELHIIAQVPPPPAAAVGACRVAVTFPLFYLATNYWILV 145
DB 239 AVLYSGVSTDEIERITEELRAFFE--PPADKA-GFVGCRVAVTVFLYPLTNNYWILV 295
QY 146 EGLYLSLIFMAFSEKKYLWGFTIIGWGLPAFVAVVWVVRATLANTGCWDLSSGHKKW 205
DB 296 EGLYLSLIFMAFSEKKYLWGFTLFGWGLPAFVAVVWVVRATLANTGCWDLSSGNKKW 355
QY 206 IIQVPILASVVLNFIPIINIRVLATKLRETNAGRCDTQOYRKLLRSTLVLVPLFGVHY 265
DB 356 IIQVPILAAIVNFIPIINIRVLATKLRETNAGRCDTQOYRKLLKSTLVLMPFGVHY 415
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAIYFCNCEVQAEIRKKSRSRWTLAL 325
DB 416 IVFMATPYTEVSGTLWQVQMHYEMLFNSFGFFVAIYFCNCEVQAEIRKKSRSRWTLAL 475
QY 326 DFRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSRLLP--ATTNGHSQLGHAK 382
DB 476 DFRRKARSGSSTSYSGPMVSHTSVTNVGPRGGLALSPLRPLAFGAGASANGHQLPGYVK 535
383 PGAPATETPLVTMAVP--KDDGFLNGSCSGLDEEASGSRPPPLIQEWETVM 435
536 HG--SISENSLPSPGPPGPKDDGYLNG--SLGYEPMVGE-QPPPLLEBERETVM 585

RESULT 6

US-08-142-551B-125
Sequence 125, Application US/08142551B
Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME

NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-7400
TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..585
OTHER INFORMATION: /note= "PTH receptor"
US-08-142-551B-125

Query Match 74.9%; Score 1710; DB 2; Length 585;
Best Local Similarity 80.2%; Pred. No. 2e-161;
Matches 333; Conservative 27; Mismatches 42; Indels 13; Gaps 7;
QY 26 EVFDRGLMIYTVGYSMASLTAVLILAYFRRLHCTRNVIHMHMFLSFMLRAASIFVKD 85
DB 179 EVFDRGLMIYTVGYSLGSLTAVLILGYFRRLHCTRNVIHMHMFLSFMLRAVSIFIKD 238
QY 86 AVLYSGTDLDEARLTFEELHIIAQVPPPPAAAVGACRVAVTFPLFYLATNYWILV 145
DB 239 AVLYSGVSTDEIERITEELRAFFE--PPADKA-GFVGCRVAVTVFLYPLTNNYWILV 295
QY 146 EGLYLSLIFMAFSEKKYLWGFTIIGWGLPAFVAVVWVVRATLANTGCWDLSSGHKKW 205
DB 296 EGLYLSLIFMAFSEKKYLWGFTLFGWGLPAFVAVVWVVRATLANTGCWDLSSGNKKW 355
QY 206 IIQVPILASVVLNFIPIINIRVLATKLRETNAGRCDTQOYRKLLRSTLVLVPLFGVHY 265
DB 356 IIQVPILAAIVNFIPIINIRVLATKLRETNAGRCDTQOYRKLLKSTLVLMPFGVHY 415
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAIYFCNCEVQAEIRKKSRSRWTLAL 325
DB 416 IVFMATPYTEVSGTLWQVQMHYEMLFNSFGFFVAIYFCNCEVQAEIRKKSRSRWTLAL 475
QY 326 DFRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSRLLP--ATTNGHSQLGHAK 382
DB 476 DFRRKARSGSSTSYSGPMVSHTSVTNVGPRGGLALSPLRPLAFGAGASANGHQLPGYVK 535

Qy 383 PGAPATETETLPVTMAVP--KDDGFLNGSCGLDEEASGSARPPLIQEGWEITVM 435
| : || : | ||||| ||||| : ||||| : |||||
Dd 536 HG--STISNSLPSGGPEPTCKDDGYLNG--SGLYEPMWGE-QPPPLLEERETVM 585

RESULT 7

US-08-869-477-6
; Sequence 6, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 58467470 No. 5846747disk of No. 5846747th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400

Query Match	74.9%;	Score 1710;	DB 2;	Length 585;
Best Local Similarity	80.2%;	Pred. No. 2e-161;		
Matches 333; Conservative	27;	Mismatches 42;	Indels 13;	Gaps 7;

Qy	26	EVFDRLGMIYTVGYSMGLASLTVAVLILAYFRRLHCTCTNYIHHMFMFVSFMLRAASIFVKD	85
Db	179	EVFDRLGMIYTVGYSLGSLTVAVLILGYFRRLHCTCTNYIHHMLFVSFMLRAVSIFIKD	238
Qy	86	AVLYSGFTLDEARLTETSELHIIIAQVPPPPAAAVGACRVATFELYFLATNYWILV	145
Db	239	AVLYSGVSTDEIRITEELRAFTET-PPPADKA-GFVGCRVAVTVELYFLTNYWILV	295
Qy	146	EGLYLHSLIFMAFPSEKKYLNGFTIFGNGLPDAVFVAWVGVRATLANTGCWDLSGGHKW	205
Db	296	EGLYLHSLIFMAFPSEKKYLNGFTIFGNGLPDAVFVAWVTVRATLANTECWDLSGGNKKW	355

206	Qy	IIQVPIIASVVLNPIILFINIRVLATKLRNAGCDTROQYRKLLRSTLVLVPLFGVHY	265
356	Db	IIQVPIIAATVWNPIILFINIRVLATKLRNAGCDTROQYRKLLKSTLVLMLPFGVHY	415
266	Qy	TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILYFCNCGEVOAIRKSWSRWTIAL	325
416	Db	IVFMATPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILYFCNCGEVOAIRKSWSRWTIAL	475
326	Qy	DFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPSLPLPP---ATTNGHSQLPGHAK	382
476	Db	DFKRRKARSGSSTYSYGPMSVHSTSVTVNGPRGLALSLSPLAPGAGASANGHHQLPGYVK	535
383	Qy	PGAPATETETLPVTMAVP--KDGFLNGSCSGLDEEASGARPPPLPQEGWETVM	435
536	Db	HSISENSLPSGSPGPGTKDQGYLNG--SGLYEPMVGE--OPPLPEEBREBETVM	595

RESIST. 8

RESULI B
US-08-468-249A-19
; Sequence 19, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-19

Query Match 74.9%; Score 1710; DB 2; Length 585;
Best Local Similarity 80.2%; Pred. No. 2e-161;
Matches 33; Conservative 27; Mismatches 42; Indels 13; Gaps 7;

QY	26	EVFDR	LGMI	YTVG	YSMS	LSLT	VAVL	ILAY	FRR	LHCT	RNTY	THM	FLS	FML	RAAS	IFVKD	85
					:					:		:		:		:	
Db	179	EVFDR	LGMI	YTVG	YSIS	LSGL	STVA	VLIG	FYRR	LHCT	RNTY	THM	FLV	SFML	RAVS	IFIKD	238
QY	86	AVLY	S	GFTL	DEAR	LTEEL	HHIA	OVPP	PPAAA	GVAG	RCV	AVTF	FLFY	FLAT	NYTW	ILV	145

Db 239 AVLYSGVSTDEIRITEELRAFT--PPADKA-GFVGCRVAVTVFLYLTNNYIWL 235
Qy 146 EGYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVAVVGVTRATLANTGCDLSSGHKKW 205
Db 296 EGYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVAVVGVTRATLANTGCDLSSGHKKW 355
Qy 206 IIQVPILASVNLFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 265
Db 356 IIQVPILAAIVNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 415
Qy 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRTAL 325
Db 416 IVFMATPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRTAL 475
Qy 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLP--ATTNGHSQLPCHAK 382
Db 476 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLP--ATTNGHSQLPCHAK 535
Qy 383 PGAPATETETLPVTMAVP--KDDGFLNGSCSGLDEEASGARPPPLLOEGMETVM 435
Db 536 HG--SISENSLPSPGPEGTCKDDOYLNG--SGLYEPMVGB-QPPPLLEBERETVM 585

RESULT 9

US-08-468-249A-18
; Sequence 18, Application US/08468249A
; Patent No. 586148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-18

Query Match 67.9%; Score 1551; DB 2; Length 515;
Best Local Similarity 86.6%; Pred. No. 1.1e-145;
Matches 291; Conservative 16; Mismatches 24; Indels 3; Gaps 2;

Qy 26 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVKD 85
Db 179 EVFDRGLMIYTVGYSMSLSGLTAVLILGFRRLHCTRNVIHMHMFLSFMRLRAASIFVKD 238
Qy 86 AVLYSGFTLDEABRLTEELHIIAQVPPPPAAAAGVAGCRVAVTVFLYLTNNYIWL 145
Db 239 AVLYSGVSTDEIRITEELRAFT--PPADKA-GFVGCRVAVTVFLYLTNNYIWL 295
Qy 146 EGYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVAVVGVTRATLANTGCDLSSGHKKW 205
Db 296 EGYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVAVVGVTRATLANTGCDLSSGHKKW 355
Qy 206 IIQVPILASVNLFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 265
Db 356 IIQVPILAAIVNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 415
Qy 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRTAL 325
Db 416 IVFMATPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRTAL 475
Qy 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSL 361
Db 476 DFKRKARSGSSSYSGPMVSHTSVTNVGPRGMPCP 511

RESULT 10
US-09-449-632-2
; Sequence 2, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jopner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 536
; ORGANISM: zebrafish
US-09-449-632-2

Query Match 64.2%; Score 1465; DB 4; Length 536;
Best Local Similarity 68.8%; Pred. No. 4.3e-137;
Matches 284; Conservative 45; Mismatches 66; Indels 18; Gaps 4;

Qy 26 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVKD 85
Db 139 EVFDRGLMIYTVGYSMSLSGLTAVLILGFRRLHCTRNVIHMHMFLSFMRLRAASIFVKD 198
Qy 86 AVLYSGFTLDEABRLTEELHIIAQVPPPPAAAAGVAGCRVAVTVFLYLTNNYIWL 145
Db 199 VLYSGSALQEMERITVEDLKSITEAPP--ANKTOFIGCKVAVTVFLYLTNNYIWL 255
Qy 146 EGYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVAVVGVTRATLANTGCDLSSGHKKW 205
Db 256 EGYLHSLIFMTFFSDRKVLMGFTLIGWGPAMFVTIWAASVRATLADTECDLSAGNLKW 315
Qy 206 IIQVPILASVNLFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 265
Db 316 IQIPIITAIIVNFIINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 375
Qy 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRTAL 325
Db 376 IVFMATPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRTAL 435
Qy 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLP--ATTNGHSQLPCHAKPGA 385

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OM protein - protein search, using sw model

Run on: July 4, 2005, 06:12:35 ; Search time 464 Seconds
(without alignments)
361.683 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGARPPPLLEGWETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2195	96.1	591	14	US-10-267-730-20
2	2187	95.8	591	9	US-09-943-446-7
3	2146	94.0	591	9	US-09-943-446-8
4	2008	88.0	593	9	US-09-943-446-9
5	2008	88.0	593	14	US-10-225-567A-229
6	2008	88.0	593	16	US-10-723-860-1006
7	2008	88.0	593	17	US-10-505-486-13
8	2002	87.7	593	10	US-09-826-509-563
9	2002	87.7	593	14	US-10-267-730-21
10	2002	87.7	593	17	US-10-925-095-563
11	1957	85.7	595	9	US-09-943-446-6

12	1710	74.9	585	14	US-10-267-730-19	Sequence 19, Appl
13	1698	74.4	964	14	US-10-017-161-710	Sequence 710, App
14	1698	74.4	964	15	US-10-292-798-622	Sequence 622, App
15	1551	67.9	515	14	US-10-267-730-18	Sequence 18, Appl
16	1465	64.2	536	14	US-10-372-095-2	Sequence 2, Appl
17	1130	49.5	542	14	US-10-372-095-4	Sequence 4, Appl
18	1068	46.8	575	14	US-10-372-095-5	Sequence 5, Appl
19	1050.5	46.0	550	14	US-10-225-567A-227	Sequence 227, App
20	1050.5	46.0	550	15	US-10-295-027-526	Sequence 526, App
21	1050.5	46.0	550	15	US-10-295-027-851	Sequence 851, App
22	1050.5	46.0	550	15	US-10-723-860-2139	Sequence 2139, App
23	1050.5	46.0	550	15	US-10-295-027-524	Sequence 524, App
24	1044.5	45.8	550	10	US-09-826-509-565	Sequence 565, App
25	1044.5	45.8	550	17	US-10-925-095-565	Sequence 565, App
26	1036	45.4	541	9	US-09-996-569-2	Sequence 2, Appl
27	1036	45.4	541	17	US-10-921-218-2	Sequence 21, Appl
28	1028.5	45.1	550	14	US-10-014-162-110	Sequence 110, App
29	1011.5	44.3	546	14	US-10-014-162-109	Sequence 109, App
30	776	34.0	459	16	US-10-831-393-4	Sequence 4, Appl
31	775.5	34.0	1324	9	US-09-935-371-56	Sequence 56, Appl
32	773.5	33.9	444	16	US-10-831-393-6	Sequence 6, Appl
33	772	33.8	459	16	US-10-831-393-3	Sequence 3, Appl
34	772	33.8	459	16	US-10-831-393-8	Sequence 8, Appl
35	762.5	33.4	458	16	US-10-831-393-5	Sequence 5, Appl
36	762.5	33.4	458	16	US-10-831-393-7	Sequence 7, Appl
37	757.5	33.2	449	15	US-10-051-874-68	Sequence 68, Appl
38	752.5	33.0	457	14	US-10-225-567A-469	Sequence 469, App
39	752.5	33.0	457	15	US-10-292-798-618	Sequence 618, App
40	752.5	33.0	457	16	US-10-831-393-1	Sequence 1, Appl
41	747	32.7	440	15	US-10-292-798-608	Sequence 608, App
42	747	32.7	440	15	US-10-051-874-64	Sequence 64, Appl
43	747	32.7	440	15	US-10-051-874-65	Sequence 65, Appl
44	747	32.7	440	15	US-10-398-454-3	Sequence 3, Appl
45	747	32.7	440	15	US-10-398-454-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-10-267-730-20
; Sequence 20, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schibani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus rattus
; US-10-267-730-20

Query Match 96.1%; Score 2195; DB 14; Length 591;
Best Local Similarity 73.6%; Pred. No. 1.5e-189;
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;

Qy	1	MGAARIAPSLALLCCPVLSAYAL	----- 25
Db	1	MGAARIAPSLALLCCPVLSAYALVDADDVFTKEQIFLLHRAQAQCDKLLKEVLHTAA	60
Qy	26	-----	25

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Db 61 NIMESDKGWTGTPASTSGKPRKEKASGKFYPESKENKDVPTGSRRRGRPCLPEDWNIVCWPL 120
Qy 26 ----- 25
Db 121 GAPGEVAVPCPDYIYDFNHKGHAYRRCDRNGSMEVVPGHNRTWANYSECLKFWMTNETRE 180
Qy 26 -EVFDRGLMIYTVGYSMASLTAVAILAYFRRLHCTRNYIHHMFSLSPMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMASLTAVAILAYFRRLHCTRNYIHHMFSLSPMLRAASIFVK 240
Qy 85 DAVLYSGFTLDEAERLTEREELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 144
Db 241 DAVLYSGFTLDEAERLTEREELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVVGVVRATLANTGCDLSSGHKK 204
Db 241 DAVLYSGFTLDEAERLTEREELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVVGVVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVVGVVRATLANTGCDLSSGHKK 360
Qy 205 WIIQVPILASVVLNFIINIRVLATKLRRETNAGRCTRQQYRKLRSTLVLVPLFGVH 264
Db 361 WIIQVPILASVVLNFIINIRVLATKLRRETNAGRCTRQQYRKLRSTLVLVPLFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWSRWTLA 324
Db 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWSRWTLA 480
Qy 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQPLGHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQPLGHAKPG 540
Qy 385 APATETETLPTVMVAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 435
Db 541 APATETETLPTVMVAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 591

RESULT 2
US-09-943-446-7
; Sequence 7, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus No. US20020146777Alvegicus
US-09-943-446-7

Query Match 95.8%; Score 2187; DB 9; Length 591;
Best Local Similarity 73.4%; Pred. No. 8e-189;
Matches 434; Conservative 0; Mismatches 1; Indels 156; Gaps 1;

Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGAARIAPSLALLCCPVLSSAYALVDADVFTKEQIFLLHRAQAQCDKLLKEVLHTAA 60
Qy 26 ----- 25
Db 61 NIMESDKGWTGTPASTSGKPRKEKASGKFYPESKENKDVPTGSRRRGRPCLPEDWNIVCWPL 120
Qy 26 ----- 25
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Db 121 GAPGEVAVPCPDYIYDFNHKGHAYRRCDRNGSMEVVPGHNRTWANYSECLKFWMTNETRE 180
Qy 26 -EVFDRGLMIYTVGYSMASLTAVAILAYFRRLHCTRNYIHHMFSLSPMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMASLTAVAILAYFRRLHCTRNYIHHMFSLSPMLRAASIFVK 240
Qy 85 DAVLYSGFTLDEAERLTEREELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 144
Db 241 DAVLYSGFTLDEAERLTEREELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVVGVVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVVGVVRATLANTGCDLSSGHKK 360
Qy 205 WIIQVPILASVVLNFIINIRVLATKLRRETNAGRCTRQQYRKLRSTLVLVPLFGVH 264
Db 361 WIIQVPILASVVLNFIINIRVLATKLRRETNAGRCTRQQYRKLRSTLVLVPLFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWSRWTLA 324
Db 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAILIYCFNGEVOAEIRKSWSRWTLA 480
Qy 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQPLGHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTNGHSQPLGHAKPG 540
Qy 385 APATETETLPTVMVAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 435
Db 541 APATETETLPTVMVAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 591

RESULT 3
US-09-943-446-8
; Sequence 8, Application US/09943446
; Patent No. US20020146777A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-943-446-8

Query Match 94.0%; Score 2146; DB 9; Length 591;
Best Local Similarity 72.1%; Pred. No. 4.1e-185;
Matches 426; Conservative 2; Mismatches 7; Indels 156; Gaps 1;

Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARAPSLALLCCPVLSSAYALVDADVFTKEQIFLLHRAQAQCDKLLKEVLHTAA 60
Qy 26 ----- 25
Db 61 NIMESDKGWTGTPASTSGKPRKEKAPGKFPESKENKDVPTGSRRRGRPCLPEDWNIVCWPL 120
Qy 26 ----- 25
Db 121 GAPGEVAVPCPDYIYDFNHKGHAYRRCDRNGSMEVVPGHNRTWANYSECLKFWMTNETRE 180
Qy 26 -EVFDRGLMIYTVGYSMASLTAVAILAYFRRLHCTRNYIHHMFSLSPMLRAASIFVK 84
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Db 181 REVFDRLGMIYTVGYSMASLTAVLILAYFRRLHCTRYNIHMHFLSFMRAASIFVK 240
Qy 85 DAVLYSGFTLDEARLTTEELHIIAQVPPPPAAAAVAGCRVAVTFEFLYFLATNYWIL 144
Db 241 DAVLYSGFTLDEARLTTEELHIIAQVPPPPAAAAVAGCRVAVTFEFLYFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFAVVAWVGVRATLANTCGWDLSSGHHK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFAVVAWVGVRATLANTCGWDLSSGHHK 360
Qy 205 WIIQVPIASVNLNFIINIRVLATKLRNAGCDTRQQYRKLRSLRVLVPLFGVH 264
Db 361 WIIQVPIASVNLNFIINIRVLATKLRNAGCDTRQQYRKLRSLRVLVPLFGVH 420
Qy 265 YTVFMAIPYEVSGTLMQIQMHYEMLFNSQGFVVAIYFCNGEVOAEIRKSWRWTLA 324
Db 421 YTVFMAIPYEVSGTLMQIQMHYEMLFNSQGFVVAIYFCNGEVOAEIRKSWRWTLA 480
Qy 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 540
Qy 385 APATETETLPTVMAVPKDDGFLNGSCSGLDEASGSARPPPLLOEGWETVM 435
Db 541 APAIENETIPTVMTVPKDDGFLNGSCSGLDEASGSARPPPLLOEGWETVM 591

RESULT 4

US-09-943-446-9

; Sequence 9, Application US/09943446

; Patent No. US2002014677A1

; GENERAL INFORMATION:

; APPLICANT: Pfizer Inc.

; APPLICANT: Castleberry, Tessa A.

; APPLICANT: Lu, Bihong

; APPLICANT: Owen, Thomas A.

; APPLICANT: Snock, Steven L.

; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor

; FILE REFERENCE: PC10891AGR

; CURRENT APPLICATION NUMBER: US/09/943,446

; CURRENT FILING DATE: 2001-08-30

; PRIOR FILING DATE: US 60/229,170

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 593

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-09-943-446-9

Query Match 88.0%; Score 2008; DB 9; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.3e-172;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;
Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLORPA 60
Qy 26 ----- 25
Db 61 SIMESDKGWTSASTSGKPRKDKASGLKYPESEEDKEAPTGSRYGRPCLPEDWHILCWPL 120
Qy 26 ----- 25
Db 121 GAFGEVAVPCPDYIYDFNKHGHAYRRCDRNGSWELVPGHNRWTWANYSECVKFLTNSTRE 180
Qy 26 ----- 25
Db 26 -EVPDRGLMIYTVGYSMASLTAVLILAYFRRLHCTRYNIHMHFLSFMRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMASLTAVLILAYFRRLHCTRYNIHMHFLSFMRAASIFVK 240
Qy 85 DAVLYSGFTLDEARLTTEELHIIAQVPPPPAAAAVAGCRVAVTFEFLYFLATNYWIL 144

Db 241 DAVLYSGATLDEARLTTEELRAIAQAPPPATAAAGYACRVAVTFEFLYFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFAVVAWVGVRATLANTCGWDLSSGHHK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFAVVAWVGVRATLANTCGWDLSSGHHK 360
Qy 205 WIIQVPIASVNLNFIINIRVLATKLRNAGCDTRQQYRKLRSLRVLVPLFGVH 264
Db 361 WIIQVPIASVNLNFIINIRVLATKLRNAGCDTRQQYRKLRSLRVLVPLFGVH 420
Qy 265 YTVFMAIPYEVSGTLMQIQMHYEMLFNSQGFVVAIYFCNGEVOAEIRKSWRWTLA 324
Db 421 YTVFMAIPYEVSGTLMQIQMHYEMLFNSQGFVVAIYFCNGEVOAEIRKSWRWTLA 480
Qy 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKP 383
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKP 540
Qy 384 GAPATET-ETLPTVMAVPKDDGFLNGSCSGLDEASGSARPPPLLOEGWETVM 435
Db 541 GTPALETLETPPMAAPKDDGFLNGSCSGLDEASGPERRPPALLOEGWETVM 593

RESULT 5

US-10-225-567A-229

; Sequence 229, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burner, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 229

; LENGTH: 593

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-229

Query Match 88.0%; Score 2008; DB 14; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.3e-172;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;
Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLORPA 60
Qy 26 ----- 25
Db 61 SIMESDKGWTSASTSGKPRKDKASGLKYPESEEDKEAPTGSRYGRPCLPEDWHILCWPL 120
Qy 26 ----- 25
Db 121 GAFGEVAVPCPDYIYDFNKHGHAYRRCDRNGSWELVPGHNRWTWANYSECVKFLTNSTRE 180
Qy 26 -EVPDRGLMIYTVGYSMASLTAVLILAYFRRLHCTRYNIHMHFLSFMRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMASLTAVLILAYFRRLHCTRYNIHMHFLSFMRAASIFVK 240
Qy 85 DAVLYSGFTLDEARLTTEELHIIAQVPPPPAAAAVAGCRVAVTFEFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEARLTTEELRAIAQAPPPATAAAGYACRVAVTFEFLYFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFAVVAWVGVRATLANTCGWDLSSGHHK 204

Db 301 VEGYLHSLIFMAFFSEKKYLWGFTVFGWGLPAVFVAVVSVRATLANTCWDLSGSKK 360
Qy 205 WIIQVPIASVNLFILFINIIRVLATKLRNAGRCRTQQRKLLRSLRVLVPLFGVH 264
Db 361 WIIQVPIASVNLFILFINIIRVLATKLRNAGRCRTQQRKLLRSLRVLVPLFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFGPFVAILIYFCNGEVOAEIRKKSWSRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQIOMHYEMLFNSFGPFVAILIYFCNGEVOAEIRKKSWSRWTLA 480
Qy 325 LDFKARKSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSOLPGHAKP 383
Db 481 LDFKARKSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSOLPGHAKP 540
Qy 384 GAPATET-ETLPTVMAVPKDDGFLNGSCGLDEASGSRPPPLLOEGWETVM 435
Db 541 GTPALETLETTPPAMAAPKDDGFLNGSCGLDEASGSRPPPALLOEGWETVM 593
RESULT 6
US-10-723-860-1006
; Sequence 1006, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10723.860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1006
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-1006

Query Match 88.0%; Score 2008; DB 16; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.3e-172;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;
Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 26 ----- 25
Db 61 SIMESDKGWTSASTSGKPRKDKASGLYPESEEDKEAPTGSRYRGRPCLPENDHILCWPL 120
Qy 26 ----- 25
Db 121 GAGEVVAVPCPDYIYDFNHKHGAYRRCDRNGSWELVPGHNRWTANYSECVKFLTNRE 180
Qy 26 -EVFDRGLMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNIIHMHFLSFMRLAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASLTVAVLILAYFRRLHCTRNIIHMHFLSFMRLAASIFVK 240
Qy 85 DAVLYSGFTLDEARLITEELHIIAQVPPPPAAAAGYACGRVAVTFFLYFLATNYYWIL 144
Db 241 DAVLYSGATLDEARLITEELRAIAQAAPPPPPATAAGYACGRVAVTFFLYFLATNYYWIL 300
Qy 145 VEGYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVVGVVRATLANTCWDLSGSKK 204
Db 301 VEGYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVVSVRATLANTCWDLSGSKK 360
Qy 205 WIIQVPIASVNLFILFINIIRVLATKLRNAGRCRTQQRKLLRSLRVLVPLFGVH 264
Db 361 WIIQVPIASVNLFILFINIIRVLATKLRNAGRCRTQQRKLLRSLRVLVPLFGVH 420

Qy 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFGPFVAILIYFCNGEVOAEIRKKSWSRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQIOMHYEMLFNSFGPFVAILIYFCNGEVOAEIRKKSWSRWTLA 480
Qy 325 LDFKARKSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSOLPGHAKP 383
Db 481 LDFKARKSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSOLPGHAKP 540
Qy 384 GAPATET-ETLPTVMAVPKDDGFLNGSCGLDEASGSRPPPLLOEGWETVM 435
Db 541 GTPALETLETTPPAMAAPKDDGFLNGSCGLDEASGSRPPPALLOEGWETVM 593
RESULT 7
US-10-505-486-13
; Sequence 13, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 13
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human
US-10-505-486-13

Query Match 88.0%; Score 2008; DB 17; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.3e-172;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;
Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 26 ----- 25
Db 61 SIMESDKGWTSASTSGKPRKDKASGLYPESEEDKEAPTGSRYRGRPCLPENDHILCWPL 120
Qy 26 ----- 25
Db 121 GAGEVVAVPCPDYIYDFNHKHGAYRRCDRNGSWELVPGHNRWTANYSECVKFLTNRE 180
Qy 26 -EVFDRGLMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNIIHMHFLSFMRLAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASLTVAVLILAYFRRLHCTRNIIHMHFLSFMRLAASIFVK 240
Qy 85 DAVLYSGFTLDEARLITEELHIIAQVPPPPAAAAGYACGRVAVTFFLYFLATNYYWIL 144
Db 241 DAVLYSGATLDEARLITEELRAIAQAAPPPPPATAAGYACGRVAVTFFLYFLATNYYWIL 300
Qy 145 VEGYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVVGVVRATLANTCWDLSGSKK 204
Db 301 VEGYLHSLIFMAFFSEKKYLWGFTIFGWGLPAVFVAVVSVRATLANTCWDLSGSKK 360
Qy 205 WIIQVPIASVNLFILFINIIRVLATKLRNAGRCRTQQRKLLRSLRVLVPLFGVH 264
Db 361 WIIQVPIASVNLFILFINIIRVLATKLRNAGRCRTQQRKLLRSLRVLVPLFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFGPFVAILIYFCNGEVOAEIRKKSWSRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQIOMHYEMLFNSFGPFVAILIYFCNGEVOAEIRKKSWSRWTLA 480

Qy 325 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383
Db 481 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLPLTATTNGHPQLPGHAKP 540
Qy 384 GAPATET-ETLPVTMAVPKDDGFLNGSCGLDEASGSRPPPLLOEGWETVM 435
Db 541 GTPALETLETPPMAAPKDDGFLNGSCGLDEASGSRPPPALLOEGWETVM 593

RESULT 8

US-09-826-509-563
; Sequence 563, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-563

Query Match 87.7%; Score 2002; DB 10; Length 593;
Best Local Similarity 67.1%; Pred. No. 4.4e-172;
Matches 398; Conservative 10; Mismatches 27; Indels 158; Gaps 3;

Qy 1 MGAARIAPSLALLCCPVLSSAYAL-----25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 26 -----25
Db 61 SIMESDKGWSASTSGKPRDKASGLYPSEEDKEAPTGSRYGRPCLPEDWHLWCPL 120
Qy 26 -----25
Db 121 GAGEVVAVPCPDYIDFNHKGHAYRRCDRNGSWELVPGHNRWTWANYSECVKFLTNRE 180
Qy 26 -EVPDRGLMIYTYGYSMSLASLTAVLILAYFRRLHCTRYNIHMHFSLFMLRAASIFVK 84
Db 181 REVFDRLGMIYTYGYSVSLASLTAVLILAYFRRLHCTRYNIHMHFSLFMLRAVSI 240
Qy 85 DAVLYSGFTLDEAERLLEEELHIIAQVPPPPAAAAGYACRVAVTPFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEAERLLEEELRAIAQAPPPATAAGYACRVAVTPFLYFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVAVGVATLANTCWDLSGCHK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVAVGVATLANTCWDLSGCHK 360
Qy 205 WIIQVPIASVNLNFIINIRVLATKLRETNAGRCDTQQYRKLLRSLTLVPLFGVH 264
Db 361 WIIQVPIASVNLNFIINIRVLATKLRETNAGRCDTQQYRKLLKSLPLVPLFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFVAILIYFCNGEVOAEIKKSWRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQVQMHYEMLFNSFGQFVAILIYFCNGEVOAEIKKSWRWTLA 480
Qy 325 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383
Db 481 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLPLTATTNGHPQLPGHAKP 540

Qy 384 GAPATET-ETLPVTMAVPKDDGFLNGSCGLDEASGSRPPPLLOEGWETVM 435
Db 541 GTPALETLETPPMAAPKDDGFLNGSCGLDEASGSRPPPALLOEGWETVM 593

RESULT 9

US-10-267-730-21
; Sequence 21, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-730-21

Query Match 87.7%; Score 2002; DB 14; Length 593;
Best Local Similarity 67.1%; Pred. No. 4.4e-172;
Matches 398; Conservative 10; Mismatches 27; Indels 158; Gaps 3;

Qy 1 MGAARIAPSLALLCCPVLSSAYAL-----25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 26 -----25
Db 61 SIMESDKGWSASTSGKPRDKASGLYPSEEDKEAPTGSRYGRPCLPEDWHLWCPL 120
Qy 26 -----25
Db 121 GAGEVVAVPCPDYIDFNHKGHAYRRCDRNGSWELVPGHNRWTWANYSECVKFLTNRE 180
Qy 26 -EVPDRGLMIYTYGYSMSLASLTAVLILAYFRRLHCTRYNIHMHFSLFMLRAASIFVK 84
Db 181 REVFDRLGMIYTYGYSVSLASLTAVLILAYFRRLHCTRYNIHMHFSLFMLRAVSI 240
Qy 85 DAVLYSGFTLDEAERLLEEELHIIAQVPPPPAAAAGYACRVAVTPFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEAERLLEEELRAIAQAPPPATAAGYACRVAVTPFLYFLATNYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVAVGVATLANTCWDLSGCHK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVAVGVATLANTCWDLSGCHK 360
Qy 205 WIIQVPIASVNLNFIINIRVLATKLRETNAGRCDTQQYRKLLRSLTLVPLFGVH 264
Db 361 WIIQVPIASVNLNFIINIRVLATKLRETNAGRCDTQQYRKLLKSLTLVPLFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFVAILIYFCNGEVOAEIKKSWRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQVQMHYEMLFNSFGQFVAILIYFCNGEVOAEIKKSWRWTLA 480
Qy 325 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383
Db 481 LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLPLTATTNGHPQLPGHAKP 540
Qy 384 GAPATET-ETLPVTMAVPKDDGFLNGSCGLDEASGSRPPPLLOEGWETVM 435

Db 541 GTPALETLETPPAMAAPKDDGFLNGSCSGLDEASGPERPPALLQBEWETVM 593

RESULT 10

US-10-925-095-563
; Sequence 563, Application US/10925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-925-095-563

Query Match	87.7%;	Score 2002;	DB 17;	Length 593;
Best Local Similarity	67.1%;	Pred. No. 4.4e-172;		
Matches	398;	Conservative 10;	Mismatches 27;	Indels 158; Gaps 3;
Qy	1	MGAARIAPSLALLCCPVLSSAYAL-----	25	
Db	1	MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEQIFLLHRAQAQCEKRLKEVLQRP	60	
Qy	26	-----	25	
Db	61	SIMESDKGWTSASTSGKPKDKASGLYPESEEDKEAPTGSRYGRPCLPENDHILCWPL	120	
Qy	26	-----	25	
Db	121	GAPGEVAVPCPDYIYDFNHKGHAYRCDRNGSWELVPGHNRWTWANYSECVKELTNETRE	180	
Qy	26	-EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYYIHMHFLSFMRAASIFVK	84	
Db	181	REVFDRLGMIYTVGYSVSLASTVAVLILAYFRRLHCTRNYYIHMHFLSFMRAVSIFVK	240	
Qy	85	DAVLYSGFTLDEAERLTERELHIIAQVPPPPAAAAGYACRVAVTFFLYFLATNYTWIL	144	
Db	241	DAVLYSGATLDEAERLTERELRAIAQAAPPPTAAAAGYACRVAVTFFLYFLATNYTWIL	300	
Qy	145	VEGLYLHSLIFMAFPSEKKYLWGFTTFGWGLPAVFVAVVWGVVVRATLANTCGWDLSSGKK	204	
Db	301	VEGLYLHSLIFMAFPSEKKYLWGFTTFGWGLPAVFVAVVWVRATLANTCGWDLSSGKK	360	
Qy	205	WIIQVPILASVVLNFIILINIRVLATKLRNAGRCDTTQQYRKLRLSTLVLVPLFGVH	264	
Db	361	WIIQVPILASVVLNFIILINIRVLATKLRNAGRCDTTQQYRKLRLSTLVLVPLFGVH	420	
Qy	265	YTVFMAIPYTVESGTLNQIQMHYEMLFNSQGFVAILIYFCNCEVQAEIRKSWRWTLA	324	
Db	421	YIVFMATPYTVESGTLNQIQMHYEMLFNSQGFVAILIYFCNCEVQAEIRKSWRWTLA	480	
Qy	325	LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATTNGHSOLPGHAKP	383	
Db	481	LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLPLPATTNGHQPQLPGHAKP	540	
Qy	384	GAPATET-ETLPVTMAYPKDDGFLNGSCSGLDEASGARPPPLLOQBEWETVM	435	
Db	541	GTPALETLETPPAMAAPKDDGFLNGSCSGLDEASGPERPPALLQBEWETVM	593	

RESULT 11

US-09-943-446-6
; Sequence 6, Application US/09943446
; Patent No. US2002014677A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Canis Familiaris
US-09-943-446-6

Query Match	85.7%;	Score 1957;	DB 9;	Length 595;
Best Local Similarity	65.8%;	Pred. No. 5.2e-168;		
Matches	394;	Conservative 11;	Mismatches 24;	Indels 172; Gaps 5;
Qy	1	MGAARIAPSLALLCCPVLSSAYAL-----	25	
Db	1	MGAVRIAPGLALLCCPVLSSAYALVDADDVMTKEQIFLLHRAQAQCKRLKEVLQRP	60	
Qy	26	-----	25	
Db	61	DIMESDKGWSASTSGKPKKEKASGLYPESEEDKEVPTGSRHRGRPCLPENDHILCWPL	120	
Qy	26	-----	25	
Db	121	GAPGEVAVPCPDYIYDFNHKGHAYRCDRNGSWELVPGHNRWTWANYSECVKELTNETRE	180	
Qy	26	-EVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRNYYIHMHFLSFMRAASIFVK	84	
Db	181	REVFDRLGMIYTVGYSVSLASTVAVLILAYFRRLHCTRNYYIHMHFLSFMRAVSIFVK	240	
Qy	85	DAVLYSGFTLDEAERLTERELHIIAQVPPPPAAAAGYACRVAVTFFLYFLATNYTWIL	144	
Db	241	DAVLYSGATLDEAERLTERELRAIAQAAPPPTAAA-GYAGCRVAVTFFLYFLATNYTWIL	299	
Qy	145	VEGLYLHSLIFMAFPSEKKYLWGFTTFGWGLPAVFVAVVWGVVVRATLANTCGWDLSSGKK	204	
Db	300	VEGLYLHSLIFMAFPSEKKYLWGFTTFGWGLPAVFVAVVWVRATLANTCGWDLSSGKK	359	
Qy	205	WIIQVPILASVVLNFIILINIRVLATKLRNAGRCDTTQQYRKLRLSTLVLVPLFGVH	264	
Db	360	WIIQVPILASVVLNFIILINIRVLATKLRNAGRCDTTQQYRKLRLSTLVLVPLFGVH	419	
Qy	265	YTVFMAIPYTVESGTLNQIQMHYEMLFNSQGFVAILIYFCNCEVQAEIRKSWRWTLA	324	
Db	420	YIVFMATPYTVESGTLNQIQMHYEMLFNSQGFVAILIYFCNCEVQAEIRKSWRWTLA	479	
Qy	325	LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSPLSPRPP-----ATTNGHSOL	377	
Db	480	LDFKRRKARSSSSSYSGPMVSHTSVTNVGPRAGLSPLSPRPLPAAAAATTATTNGHPP	539	
Qy	378	PGHAKPGAPATETETLPVT---NAVPRKDDGFLNGSCSGLDEASGARPPPLLOQBEWETV	434	
Db	540	PGHTKFGAP-----TLPATPPATAAPKDDGFLNGSCSGLDEASAPERPALLQBEWETV	594	
Qy	435	M 435		
Db	595	M 595		

RESULT 12

US-10-267-730-19
; Sequence 19, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-19

Query Match 74.9%; Score 1710; DB 14; Length 585;
Best Local Similarity 80.2%; Pred. No. 1.1e-145;
Matches 333; Conservative 27; Mismatches 42; Indels 13; Gaps 7;

Qy 26 EVFDRGMIVTVGYSMASLTAVLILAYPRRLHCTRNTHMFLFVSMRAASIFVKD 85
Db 179 EVFDRGMIVTVGYSSISGLSTVAVLILGYPRRLHCTRNTHMFLFVSMRAASIFIKD 238

Qy 86 AVLYSGTDLDEAERLITEELHIIAQVPPPPAAAAGVAGCEVATFPLFLATNYWILV 145
Db 239 AVLYSGVSTDEIERITEELRAFTF--PPPADKA-GFVGCKVAVTVFLYLTNYWILV 295

Qy 146 EGLYHSLIFMAFFSEKKYLGFTIFGWLPAVFAVAVVAVRATLANTGWDLSGGHKW 205
Db 296 EGLYHSLIFMAFFSEKKYLGFTIFGWLPAVFAVAVVAVRATLANTGWDLSGGKNW 355

Qy 206 IIQVPILASVNLFINIRVATKLRETNAGRCDTQQYRKLRLSTLVLPLFGVHY 265
Db 356 IIQVPILAAIIVNFIINIRVATKLRETNAGRCDTQQYRKLRLSTLVLPLFGVHY 415

Qy 266 TVFMALPYTEVSGTLQIOMHYEMLFNSFQGFVVAIIYFCNGEVQAEIRKSWSRWTL 325
Db 416 IVFMATPYTEVSGTLQVQMHYEMLFNSFQGFVVAIIYFCNGEVQAEIRKSWSRWTL 475

Qy 326 DFKKRARGSSSYSGPMVSHTSVTNVPGRAGLSPLSPRLPP---ATTNGHSOLPGHAK 382
Db 476 DFKKRARGSSSYSGPMVSHTSVTNVPGRGLALSPLAPGAGASANGHQLPGYVK 535

Qy 383 PGAPATETLTPLVTMAVP--KDDGFLNGSCSGLDEEASGSARPPPLQEGWETVM 435
Db 536 HG--SISENSLPSSGPEPGTKDDGYLNG--SGLYEPMVGE-QPPPLLEERETVM 585

RESULT 13

US-10-017-161-710
; Sequence 710, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18

; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 710
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-710

Query Match 74.4%; Score 1698; DB 14; Length 964;
Best Local Similarity 59.9%; Pred. No. 2.6e-144;
Matches 356; Conservative 11; Mismatches 31; Indels 196; Gaps 9;

Qy 26 EVFDRGMIVTVGYSMASLTAVLILAYF-----RRHCTRNTHMFLFVSMRAASIF 56
Db 317 EVFDRGMIVTVGYSVSLASTVAVLILAYFRWAGRGERRRDMVEGGRWPRSDATPSLHP 376

Qy 57 -----
Db 377 SPFAGVPTYGAQSPFLSTHRASPCPHRSCRAPRRRLHCTRNTHMFLFVSMRAASIF 436

Qy 83 VKDAVLYSGTDLDEAERLITEELHIIAQVPPPPAAAAGVAG----- 124
Db 437 VKDAVLYSGATLDEAERLITEELRAIAQAAPPATAAAGVSTPLPARSCRHWPRGAPP 496

Qy 125 -----CR----- 126
Db 497 RPAPARSPCPPASATGFSHNSPVSVPNPNQCRPCQGLRVSHSTPRAAIKAPTSTQ 556

Qy 127 VAVTFPLFLATNYWILVEGLYLHSLIFMAFFSEKKYLGFTIFGWLPAVFAVAVVGV 186
Db 557 VAVTFPLFLATNYWILVEGLYLHSLIFMAFFSEKKYLGFTIFGWLPAVFAVAVVSV 616

Qy 187 RATLANAGCWDLSGGHKWIIQVPIIASVV--LNFILFINIRVATKLRETNAGRCDT 244
Db 617 RATLANAG-----VQPPDAAPSLPQLNFILFINIRVATKLRETNAGRCDT 664

Qy 245 QQY-----RKLRLSTLVLPLFGVHYTVFMALPYTEVSGTLQIOMHYEML 290
Db 665 QQYRGSGALTYLPRPRKLLKSTLVLPLFGVHYIVFMATPYTEVSGTLQVQMHYEML 724

Qy 291 FNSF-----QGFVVAIIYFCNGEVQAEIRKSWSRWTL 323
Db 725 FNSFQVRSAGPLAEGRGSGRPSDRHPSQGFVVAIIYFCNGEVQAEIRKSWSRWTL 784

Qy 324 ALDFKKRARGSSSYSGPMVSHTSVTNVPGRAGLSPLSPRLPP---LPPATTNGHSOLPGHAK 382
Db 785 ALDFKKRARGSSSYSGPMVSHTSVTNVPGRVGLGLPLSPRLPPTATTNGHPLPGHAK 844

Qy 383 PGAPATET-ETLPLVTMAVPKDDGFLNGSCSGLDEEASGSARPPPLQEGWETVM 435
Db 845 PGTPALETLETTTPPMAAPKDDGFLNGSCSGLDEEASGPRPPALLQEEWETVI 898

RESULT 14

US-10-292-798-622
; Sequence 622, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 622
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-292-798-622

Query Match      74.4%; Score 1698; DB 15; Length 964;
Best Local Similarity 59.9%; Pred. No. 2.6e-144;
Matches 356; Conservative 11; Mismatches 31; Indels 196; Gaps 9;

Qy 26 EVFDRGLMIYTVGYSMSLASLTAVAILAYF----- 56
Db 317 EVFDRGLMIYTVGYSMSLASLTAVAILAYFRWAGRRRRDVEGGRWPRSDATPSLHP 376
Qy 57 -----RRLHCTRNTHMMFLSFMRLRAASIF 82
Db 377 SPPAGVPTYGAQPSFLSTRASPCPHRSCRAPRRRLHCTRNTHMHLFLSFMRLRAVSIF 436
Qy 83 VKDAVLYSGFTLDEAERLITEELHIIAQVPPPPAAAAAGVAG----- 124
Db 437 VKDAVLYSGATLDEAERLITEELRAIAOAPPPATAAAGTVSTPLPARSCRHWPRGAPP 496
Qy 125 -----CR----- 126
Db 497 RPAPARSPCPPASATGFSHNSPSYRVPRNPQLCRPPCCQLRVSHSTPRAAIKAPTSTQ 556
Qy 127 VAVTFFLYFLATNYWTLVEGLYHLSLI FMAFFSEKKYLMGFTIFGWLPAVFAVAVWVG 186
Db 557 VAVTFFLYFLATNYWTLVEGLYHLSLI FMAFFSEKKYLMGFTIFGWLPAVFAVAVWVS 616
Qy 187 RATLANTGCDLSSGHKKWIIQVPIASVV--LNFIILFINIIRVLATKLRETNAGRCDDR 244
Db 617 RATLANTG-----VQPPDAAPSLPQLNFILFINIIRVLATKLRETNAGRCDDR 664
Qy 245 QQY-----RKLLRSTLVLPVLFVGHVYTVFMALPYTEVSGTLWQIQMHYEM 290
Db 665 QQYRGSGSLATYLPWPRLKLLKSTLVLMPLFGVHYIVFMATPYTEVSGTLWQVQMHYEM 724
Qy 291 FNSF-----QQFFVAILIYFCNGEVOAEIRKSWSRWTL 323
Db 725 FNSFQVRSAGPLAEGRGSGRSDSRHPSQSGFFVAILIYFCNGEVOAEIRKSWSRWTL 784
Qy 324 ALDFKRRKARSGSSSYSGPMVSHSTVTVNGPRAGLSLPLSPR-LPPATTNGHSQLPGHAK 382
Db 785 ALDFKRRKARSGSSSYSGPMVSHSTVTVNGPRVGLGLPLSPRLPLPTATTNGHPQLPGHAK 844
Qy 383 PGAPATET-ETLPTVMAVPKDDGLNGSCSGLDEEASGSARPPPLQLQEGWETVM 435
Db 845 PGTPALETLETPPMAAPKDDGDLNGSCSGLDEEASGSPRPALLQEEWETVI 898

RESULT 15
US-10-267-730-18
; Sequence 18, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
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; TYPE: PRT
; ORGANISM: Didelphoidea
; US-10-267-730-18

Query Match      67.9%; Score 1551; DB 14; Length 515;
Best Local Similarity 86.6%; Pred. No. 2.3e-131;
Matches 291; Conservative 18; Mismatches 24; Indels 3; Gaps 2;

Qy 26 EVFDRGLMIYTVGYSMSLASLTAVAILAYFRLHCTRNTHMHLFVSEMLRAASIFVKD 85
Db 179 EVFDRGLMIYTVGYSMSLASLTAVAILAYFRLHCTRNTHMHLFVSEMLRAVSIFIKD 238
Qy 86 AVLYSGFTLDEAERLITEELHIIAQVPPPPAAAAAGVAGCRVAVTFPFLYFLATNYWILV 145
Db 239 AVLYSGVSTDEIERITEELRAFTE--PPADKA-GFVGCRAVTVFLYFLATNYWILV 295
Qy 146 EGYLHSLIFMAPFSEKKYLMGFTIFGWLPAVFAVAVWVGVRATLANTGCWDLSSGHKKW 205
Db 296 EGYLHSLIFMAPFSEKKYLMGFTIFGWLPAVFAVAVWVTRATLANTECWDLSSGNKKW 355
Qy 206 IIQVPILASVVLNFILFINIIRVLATKLRETNAGRCDDRQOYRKLLRSTLVLPFGVHY 265
Db 356 IIQVPILAAIVNFIILFINIIRVLATKLRETNAGRCDDRQOYRKLLKSTLVLMPLFGVHY 415
Qy 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWSRWTLAL 325
Db 416 IVFMATPYTEVSGTLWQVQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWSRWTLAL 475
Qy 326 DFKRRKARSGSSSYSGPMVSHSTVTVNGPRAGLSLP 361
Db 476 DFKRRKARSGSSSYSGPMVSHSTVTVNGPRGWP 511
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Search completed: July 4, 2005, 06:27:00
Job time : 467 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2005, 04:26:48 ; Search time 24 Seconds
(without alignments)
1743.929 Million cell updates/sec

Title: US-09-869-565-2
Perfect score: 2283
Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGSARPPPLQEGWETVM 435

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2187	95.8	591	2	I54195
2	2146	94.0	591	2	S44203
3	2134	93.5	589	2	I59297
4	2008	88.0	593	2	A49191
5	1710	74.9	585	2	A39286
6	1050.5	46.0	550	2	A57519
7	772	33.8	459	2	JH0594
8	757.5	33.2	449	2	S16319
9	745	32.6	440	2	JC2532
10	741	32.5	460	2	JC2194
11	741	32.5	495	2	JC2195
12	687	30.1	525	2	JN0902
13	684	30.0	467	2	JN0616
14	676.5	29.6	437	2	JU0185
15	672.5	29.5	437	2	S39069
16	671	29.4	381	2	S33449
17	671	29.4	495	2	S39061
18	671	29.4	495	2	S36114
19	666	29.2	438	2	G02822
20	666	29.2	513	2	S47631
21	657	28.8	523	2	S39060
22	649	28.4	462	2	JC2462
23	634.5	27.8	466	2	G02334
24	634.5	27.8	466	2	S66676
25	613.5	26.9	455	2	I53273
26	604	26.5	463	2	A46172
27	597.5	26.2	491	2	I37411
28	595.5	26.1	485	2	JQ1957
29	594	26.0	463	2	S71624

30	592	25.9	463	2	I84494
31	582.5	25.5	485	2	JC4363
32	571.5	25.0	477	2	JC2041
33	567.5	24.9	423	2	A45363
34	567.5	24.9	451	2	I46586
35	560.5	24.6	423	2	S29753
36	535	23.4	464	2	S29754
37	521	22.8	515	2	I60800
38	518	22.7	479	2	S33746
39	514.5	22.5	515	2	I49154
40	512	22.4	474	2	I37217
41	511.5	22.4	478	2	A37430
42	497	21.8	490	2	S34486
43	488	21.4	482	2	A39285
44	476	20.8	461	2	JC2477
45	476	20.8	498	2	I47130

ALIGNMENTS

RESULT 1

I54195
parathyroid hormone/parathyroid hormone related-peptide receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I54195; A42698
R;Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier
Genomics 20, 20-26, 1994
A;Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (I54195) and rat genomes.
A;Reference number: I54195; MUID:94292182; PMID:8020952
A;Accession: I54195
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-591 <RES>
A;Cross-references: UNIPROT:P25961; GB:I19475; NID:94673116; PIDN:AAA68098.1; PID:94673117
R;Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure
Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
A;Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid
n of both cAMP and inositol trisphosphates and increases intracellular free calcium.
A;Reference number: A42698; MUID:92212903; PMID:1313566
A;Accession: A42698
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-585, 'G', 587-591 <ABO>
A;Experimental source: ROS 17/2.8 osteosarcoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:92187)
C;Superfamily: glucagon receptor

Query Match	95.8%	Score 2187;	DB 2;	Length 591;
Best Local Similarity	73.4%	Pred. No. 3.4e-174;		
Matches	434;	Conservative	0;	Mismatches 1;
Indels	156;	Gaps	1;	
Qy	1	MGAARIAPSLALLCCPVLSAYAL-----	25	
Db	1	MGAARIAPSLALLCCPVLSAYALVDDVFTKBEQIFLLHRAQAQCDKLLKEVLHTAA	60	
Qy	26	-----	25	
Db	61	NIMESDKGWTTPASTSGKPRKEKASGFYPESKENKDVPTGSRRRGRPCLPEDWNIVCWPL	120	
Qy	26	-----	25	
Db	121	GAPGEVVAVPCPDYIYDFNHKGHAYRRCDSNGSWEVVPVGHNRWTWANYSECLKFWMTNETRE	180	
Qy	26	-EVFDRGLMIYTVGYGSMISLASLTAVLILAYFRRLHCTRYNIHMHFLSFMRLRAASIFVK	84	
Db	181	REVFDRLGMIYTVGYGSMISLASLTAVLILAYFRRLHCTRYNIHMHFLSFMRLRAASIFVK	240	
Qy	85	DAVLVSGFTLDEAERLTTEELHIIAQVPPPPAAAGYACGRVATFEFLFLATNTYMWIL	144	
Db	241	DAVLVSGFTLDEAERLTTEELHIIAQVPPPPAAAGYACGRVATFEFLFLATNTYMWIL	300	

Db 539 APAIENETIPVTWTPKDDGFLNGSCSGLDEASGSARPPPLQEWETVM 589

RESULT 4

A49191

parathyroid hormone/PTH-related peptide receptor - human

N;Alternate names: parathyroid hormone/parathyroid hormone related peptide receptor

C;Species: Homo sapiens (man)

C;Date: 19-Dec-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: I38139; A49191; I38113; G01562; S29610

R;Schipani, E.; Weinstein, I.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuurmann, M.

Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Jueppner, H.

J. Clin. Endocrinol. Metab. 80, 1611-1621, 1995

A;Title: Pseudohypoparathyroidism type IB is not caused by mutations in the coding exons

A;Reference number: I38139; MUID:95263723; PMID:7745008

A;Accession: I38139

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-593 <RES>

A;Cross-references: UNIPROT:Q03431; EMBL:U22409; NID:9897594; PIDN:AAB60657.1; PID:98975

R;Schipani, E.; Karga, H.; Karaplis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V.

Endocrinology 132, 2157-2165, 1993

A;Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pa

A;Reference number: A49191; MUID:93238641; PMID:8386612

A;Accession: A49191

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-593 <CH>

A;Cross-references: GB:104308; NID:g190721; PIDN:AAA36525.1; PID:g190722

A;Note: sequence extracted from NCBI backbone (NCBIN:130233, NCBIPI:130234)

R;Schneider, H.; Feyen, J.H.; Seuwen, K.; Movva, N.R.

Eur. J. Pharmacol. 246, 149-155, 1993

A;Title: Cloning and functional expression of a human parathyroid hormone receptor.

A;Reference number: I38113; MUID:93387403; PMID:8397094

A;Accession: I38113

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-593 <RE2>

A;Cross-references: EMBL:X68596; NID:g396812; PIDN:CAA48589.1; PID:g396813

R;Levine, M.

submitted to the EMBL Data Library, November 1994

A;Reference number: G07787

A;Accession: G01562

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-593 <LEV>

A;Cross-references: EMBL:U17418; NID:g596129; PIDN:AAA56774.1; PID:g596130

C;Genetics:

A;Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 45

C;Superfamily: glucagon receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 88.0%; Score 2008; DB 2; Length 593;

Best Local Similarity 67.3%; Pred. No. 2.8e-159;

Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

Qy 1 MGAARIAPSLALCCPVLSAYAL----- 25

Db 1 MGTARIAPGLALCCPVLSAYALVDADVMTKEEQIFLHRAQAQCEKKLKEVLORPA 60

Qy 26 ----- 25

Db 61 SIMESDKWTSASTSGKPRKDKASGLKYPESEEDKEAPTGSRYGRPCLPEDWHLWCPL 120

Qy 26 ----- 25

Db 121 GAPGEWAVPCPDYIDFNHKGHAYRCDRNGSWELVPGHNRTWANYSECVKFLTNRE 180

Qy 26 -EVDRLGMIYTCVGSNSLASLTAVALLAYFRRLHCTRNTHMHMFLSFMRLRAASIFVK 84

Db 181 REVDRLGMIYTCVGSNSLASLTAVALLAYFRRLHCTRNTHMHMFLSFMRLRAVSI 240

Qy 85 DAVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAAGVAGCRVAVTFFLYLATNYWIL 144

Db 241 DAVLYSGATLDEAERLTHEELRAIAQAPPPATAAGYACRVAVTFFLYLATNYWIL 300

Qy 145 VEGLYLHSLIFMAFFSEKKYLWGFTTFGWGLPAVFAVAVVGVVRATLANTCWDLSGGHK 204

Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTTFGWGLPAVFAVAVVGVVRATLANTCWDLSGNKK 360

Qy 205 WIIQVPIASVILNFILFINIRVLATKURETNAGRCDDTQQYRKLLRSTLVLPFGVH 264

Db 361 WIIQVPIASVILNFILFINIRVLATKURETNAGRCDDTQQYRKLLKSTLVLPFGVH 420

Qy 265 YTFMALPYTEVSGTLWQIMHYEMLFNSFGQFVAIIYCFNGEVOAEIRKSWRWTLA 324

Db 421 YIVFMATPYTEVSGTLWQIMHYEMLFNSFGQFVAIIYCFNGEVOAEIRKSWRWTLA 480

Qy 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATTNGHSOLPGHAKP 383

Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRVGLGULPLSPRLPTATTNGHQLPGHAKP 540

Qy 384 GAPATET-ETLPVTMAVPKDDGFLNGSCSGLDEASGSARPPPLQEWETVM 435

Db 541 GTPALETLETPPAMAAPKDDGFLNGSCSGLDEASGPERPPALQEWETVM 593

RESULT 5

A39286

parathyroid hormone / parathyroid hormone-related peptide - North American opossum

C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)

C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004

C;Accession: A39286

R;Jueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.; K

Science 254, 1024-1026, 1991

A;Title: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-rel

A;Reference number: A39286; MUID:92054592; PMID:1658941

A;Accession: A39286

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-585 <JUE>

A;Cross-references: UNIPROT:P25107; GB:M74445

C;Superfamily: glucagon receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 74.9%; Score 1710; DB 2; Length 585;

Best Local Similarity 80.2%; Pred. No. 1.8e-134;

Matches 333; Conservative 27; Mismatches 42; Indels 13; Gaps 7;

Qy 26 EVDRLGMIYTCVGSNSLASLTAVALLAYFRRLHCTRNTHMHMFLSFMRLRAASIFVKD 85

Db 179 EVDRLGMIYTCVGSNSLSGLTAVALLAYFRRLHCTRNTHMHMFLSFMRLRAVSIIFIKD 238

Qy 86 AVLYSGFTLDEAERLTHEELHIIAQVPPPPAAAAAGVAGCRVAVTFFLYLATNYWILV 145

Db 239 AVLYSGVSTDEIERITHEELRAGTE--PPADKA-GFVGCRVAVTFFLYLATNYWILV 295

Qy 146 EGYLYHSLIFMAFFSEKKYLWGFTTFGWGLPAVFAVAVVGVVRATLANTCWDLSGGHKW 205

Db 296 EGYLYHSLIFMAFFSEKKYLWGFTTFGWGLPAVFAVAVVGVVRATLANTCWDLSGNKKW 355

Qy 206 IIOVPIASVILNFILFINIRVLATKURETNAGRCDDTQQYRKLLRSTLVLPFGVHY 265

Db 356 IIOVPIAAIVANFILFINIRVLATKURETNAGRCDDTQQYRKLLRSTLVLPFGVHY 415

Qy 266 TVFMALPYTEVSGTLWQIMHYEMLFNSFGQFVAIIYCFNGEVOAEIRKSWRWTLAL 325

Db 416 IVFMATPYTEVSGTLWQIMHYEMLFNSFGQFVAIIYCFNGEVOAEIRKSWRWTLAL 475

Qy 326 DFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPRLPP---ATTNGHSOLPGHAK 382

Db 476 DFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPRLAPGAGASANGHQLPGYVK 535

Qy 383 PGAPATETPLVTMAVP--KDDGFLNGSCSGLDEASGSARPPPLQEWETVM 435

Db 536 HG--SISENSLPSSGPEFGTKDDGYLNG--SGLYEPMVGE--QPPPLLEERETVM 585

RESULT 6
A57519
Parathyroid hormone receptor 2 precursor - human
N/A: Altername names: PH2 receptor
C/Species: Homo sapiens (man)
C/Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
C/Accession: A57519
R/Usdin, T.B.; Gruber, C.; Bonner, T.I.
J. Biol. Chem. 270, 15455-15458, 1995
A/Title: Identification and functional expression of a receptor selectively recognizing
A/Reference number: A57519; MUID:95318121; PMID:7797535
A/Accession: A57519
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-550 <USD>
A/Cross-references: UNIPROT:P49190; GB:U25128; NID:g9887966; PIDN:AAC50157.1; PID:g9887967
C/Genetics:
A/Map position: 2q33-2q33
A/Map position: 2q33-2q33
C/Superfamily: glucagon receptor
C/Keywords: hormone receptor

Query Match 46.0%; Score 1050.5; DB 2; Length 550;
Best Local Similarity 53.9%; Pred. No. 1.4e-79;
Matches 208; Conservative 58; Mismatches 85; Indels 35; Gaps 7;
Qy 26 EVFRLGMIYTVGYSMSLASLTVAVLILAYFRLHCTRNTHMHMFLSFMRLRAASIFVKD 85
Db 139 EFFERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRNTHMHLFVSFMRATSIKVD 198
Qy 86 AVLYSGFTDABRLTEELHIIAQVPPPPAAAAGV-----YACRVAVTFEFLYFATNY 140
Db 199 RVHAHIGVKELES-----IQDDPQNSIETSVDKSYIGCKIAVWFIYFLATNY 251
Qy 141 YWILVEGLYLHSLIFMAFFSEKKYLGWFTIFGWLPAFVAVVGVATLANTGCDLSS 200
Db 252 YWILVEGLYLHNLIFVAFPSDTKYLWGFILGWGFPAAFAVAVARATLADARCWLSA 311
Qy 201 GHKWIIOVPLASVNLFINIIRVLATKLRETNAGRCDTQOYRKLRLSTLVLVPL 260
Db 312 GDIKWIQAPILAAIGLNFILFNLTVRLATKIWETNAVGHTRKQYRKLAKSTLVLV 371
Qy 261 FGVIHYTFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVAILIYFCNGEVOAEIRKWSR 320
Db 372 FGVIHYTFVCLPHS-FTGLGWEIRMHCELPFNSFGQFFVAILIYFCNGEVOAEIRKWSR 430
Qy 321 WTALDPKPKARSGS-----SSYSYSGPMVSHTSVTNVGPRAGLSPLSPRLPP 368
Db 431 WNLSDVWKRTPPCGSRRCGSLVLTVTHTSTSSQVAASTRWLI---SGKAATIASRQP- 486
Qy 369 ATTNGHSQLCHAKGAPATETILP 394
Db 487 ---DSHTITLPGYWSN---SEQDCLP 506

RESULT 7
JH0594
vasoactive intestinal peptide receptor precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C/Accession: JH0594; S56014
R/Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.
Neuron 8, 811-819, 1992
A/Title: Functional expression and tissue distribution of a novel receptor for vasoactive
A/Reference number: JH0594; MUID:92232309; PMID:1314625
A/Accession: JH0594
A/Molecule type: mRNA
A/Residues: 1-459 <ISH>
A/Cross-references: UNIPROT:P30083; GB:M86835; NID:g207640; PIDN:AAA42331.1; PID:g207641
A/Experimental source: lung

Query Match 46.0%; Score 1050.5; DB 2; Length 550;
Best Local Similarity 53.9%; Pred. No. 1.4e-79;
Matches 208; Conservative 58; Mismatches 85; Indels 35; Gaps 7;
Qy 26 EVFRLGMIYTVGYSMSLASLTVAVLILAYFRLHCTRNTHMHMFLSFMRLRAASIFVKD 85
Db 139 EFFERLYVMYTVGYSISFGSLAVAILIIGYFRLHCTRNTHMHLFVSFMRATSIKVD 198
Qy 86 AVLYSGFTDABRLTEELHIIAQVPPPPAAAAGV-----YACRVAVTFEFLYFATNY 140
Db 199 RVHAHIGVKELES-----IQDDPQNSIETSVDKSYIGCKIAVWFIYFLATNY 251
Qy 141 YWILVEGLYLHSLIFMAFFSEKKYLGWFTIFGWLPAFVAVVGVATLANTGCDLSS 200
Db 252 YWILVEGLYLHNLIFVAFPSDTKYLWGFILGWGFPAAFAVAVARATLADARCWLSA 311
Qy 201 GHKWIIOVPLASVNLFINIIRVLATKLRETNAGRCDTQOYRKLRLSTLVLVPL 260
Db 312 GDIKWIQAPILAAIGLNFILFNLTVRLATKIWETNAVGHTRKQYRKLAKSTLVLV 371
Qy 261 FGVIHYTFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVAILIYFCNGEVOAEIRKWSR 320
Db 372 FGVIHYTFVCLPHS-FTGLGWEIRMHCELPFNSFGQFFVAILIYFCNGEVOAEIRKWSR 430
Qy 321 WTALDPKPKARSGS-----SSYSYSGPMVSHTSVTNVGPRAGLSPLSPRLPP 368
Db 431 WNLSDVWKRTPPCGSRRCGSLVLTVTHTSTSSQVAASTRWLI---SGKAATIASRQP- 486
Qy 369 ATTNGHSQLCHAKGAPATETILP 394
Db 487 ---DSHTITLPGYWSN---SEQDCLP 506

R/Pei, L.; Melmed, S.
Biochem. J. 308, 719-723, 1995
A/Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene 5'
A/Reference number: S56014; MUID:97104266; PMID:8948424
A/Accession: S56014
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-26 <PBI>
A/Cross-references: EMBL:U10635; NID:g505752; PIDN:AAB48185.1; PID:g514311
C/Superfamily: glucagon receptor
C/Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein
F/1-30/Domain: signal sequence #status predicted <SIG>
F/31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <MAT>
F/146-168/Domain: transmembrane #status predicted <TM1>
F/176-195/Domain: transmembrane #status predicted <TM2>
F/218-241/Domain: transmembrane #status predicted <TM3>
F/256-277/Domain: transmembrane #status predicted <TM4>
F/295-318/Domain: transmembrane #status predicted <TM5>
F/344-363/Domain: transmembrane #status predicted <TM6>
F/376-395/Domain: transmembrane #status predicted <TM7>
F/58,69,100,292/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 33.8%; Score 772; DB 2; Length 459;
Best Local Similarity 44.8%; Pred. No. 1.7e-56;
Matches 147; Conservative 64; Mismatches 83; Indels 34; Gaps 7;
Qy 35 YTVGYSMSLASLTVAVLILAYFRLHCTRNTHMHMFLSFMRLRAASIFVKDVLVSGFTL 94
Db 147 YTVGYSMSLASLTVAVLILAYFRLHCTRNTHMHMFLSFMRLRAASIFVKDVLVSGFTL 206
Qy 95 DEARLITEBELHIIAQVPPPPAAAAGVACRVAVTFEFLYFATNYWILVEGLYLHSLI 154
Db 207 DHCSEAS-----VGCKAAVVFQYCVMANEFLLVLEGLYLYTL 245
Qy 155 FMAFFSEKKYLGWFTIFGWLPAFVAVVGVATLANTGCD-LSGCHKWIIQVPILA 213
Db 246 AVSFSEKKYLGWFTIFGWLPAFVAVVGVATLANTGCD-LSGCHKWIIQVPILA 305
Qy 214 SVVNLFINIIRVLATKLRETNAGRCDTQOYRKLRLSTLVLVPLFGVHYTVFVMA 273
Db 306 SILVNFVLCIIRILVQLRPPDIGNDS-SPYSRLAKSTLILPLFGVHYVMAFFP- 363
Qy 274 TEVSGTLWQIOMHYEMLFNSFGQFFVAILIYFCNGEVOAEIRKWSRWTI--ALDPKPKA 331
Db 364 ---DNFAQVQVVFELVWGSFGQFFVAILIYFCNGEVOAEIRKWSRWTI--ALDPKPKA 420
Qy 332 R---SGSSSYSGPMVSHTSVTNVGPR 356
Db 421 QHPWGSNGATCSTQVS--MLTRVSPSA 446

RESULT 8
S16319
secretin receptor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S16319
R/Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.
EMBO J. 10, 1635-1641, 1991
A/Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.
A/Reference number: S16319; MUID:91266890; PMID:1646711
A/Accession: S16319
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-449 <ISH>
A/Cross-references: UNIPROT:P23811; EMBL:X59132; NID:g57228; PIDN:CAA41849.1; PID:g57229
C/Superfamily: glucagon receptor
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 33.2%; Score 757.5; DB 2; Length 449;
Best Local Similarity 44.8%; Pred. No. 2.7e-55;
Matches 154; Conservative 64; Mismatches 87; Indels 39; Gaps 9;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2005, 02:53:08 ; Search time 90 Seconds
(without alignments)
2475.049 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSLALLCCPVLS.....EAGSARPPPLQEGWETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2187	95.8	591	1 PTHR_RAT	P25961 rattus norv
2	2156	94.4	591	2 Q80W08	Q80W08 mus musculu
3	2148	94.1	591	2 Q91WV4	Q91WV4 mus musculu
4	2146	94.0	591	1 PTHR_MOUSE	P41593 mus musculu
5	2008	88.0	593	1 PTHR_HUMAN	Q03431 homo sapien
6	1957	85.7	595	2 Q9TUJ1	Q9TUJ1 canis famil
7	1932	84.6	589	2 Q7YR13	Q7YR13 cervus elap
8	1925	84.3	585	1 PTHR_PIG	P50133 sus scrofa
9	1710	74.9	585	1 PTHR_DIDWA	P25107 didelphis m
10	1698	74.4	964	2 Q8NH54	Q8NH54 homo sapien
11	1465	64.2	536	2 Q9PVD3	Q9PVD3 brachydanio
12	1151	50.4	542	2 Q9PVD2	Q9PVD2 brachydanio
13	1078	47.2	575	2 Q9PWB7	Q9PWB7 brachydanio
14	1050.5	46.0	550	1 PTHR2_HUMAN	P49190 homo sapien
15	1011.5	44.3	546	1 PTHR2_RAT	P70555 rattus norv
16	1006.5	44.1	546	1 PTHR2_MOUSE	Q91V95 mus musculu
17	991	43.4	589	2 Q9GMD1	Q9GMD1 oryctolagus
18	777	34.0	147	2 Q76N28	Q76N28 rattus norv
19	776	34.0	459	1 VIPR_MOUSE	P97751 mus musculu
20	773.5	33.9	444	2 Q9YH66	Q9YH66 rana ridibu
21	772	33.8	459	1 VIPR_RAT	P30083 rattus norv
22	762.5	33.4	458	1 VIPR_PIG	Q28992 sus scrofa
23	757.5	33.2	449	1 SCRC_RAT	P23811 rattus norv
24	752.5	33.0	457	1 VIPR_HUMAN	P32241 homo sapien
25	749.5	32.8	445	1 SCRC_RABIT	O46502 oryctolagus
26	747	32.7	440	1 SCRC_HUMAN	P47872 homo sapien
27	746.5	32.7	457	2 Q6P2M6	Q6P2M6 homo sapien
28	746	32.7	440	2 Q81V17	Q81V17 homo sapien
29	743	32.5	419	2 Q8AXV4	Q8AXV4 fugu rubrip
30	729	31.9	457	1 VIPR_MEIGA	Q91085 meleagris g
31	728	31.9	419	2 Q8AXV3	Q8AXV3 fugu rubrip

32	725	31.8	418	2 Q9IBG2	Q9IBG2 gallus gall
33	718	31.4	447	1 VIPR_CARAU	Q90308 carassius a
34	698	30.6	465	2 Q73769	Q73769 carassius a
35	687	30.1	468	1 PACR_HUMAN	P41586 homo sapien
36	683	29.9	435	2 Q64FL3	Q64FL3 oncorhynch
37	681.5	29.9	437	2 Q6PRD2	Q6PRD2 cavia porce
38	681.5	29.9	437	2 Q6PRD3	Q6PRD3 cavia porce
39	680	29.8	459	2 Q8BGA4	Q8BGA4 m mus muscu
40	680	29.8	465	2 Q9PTK1	Q9PTK1 xenopus lae
41	680	29.8	468	2 Q6NXJ9	Q6NXJ9 mus musculu
42	679	29.7	457	2 Q64FL5	Q64FL5 oncorhynch
43	676.5	29.6	437	1 VIPS_MOUSE	P41588 mus musculu
44	674	29.5	455	2 Q90Y10	Q90Y10 rana ridibu
45	672.5	29.5	437	1 VIPS_RAT	P35000 rattus norv

ALIGNMENTS

RESULT 1

ID	PTRR_RAT	STANDARD;	PRT;	591 AA.
AC	P25961;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Parathyroid hormone/parathyroid hormone-related peptide receptor			
DE	precursor (PTH/PTHr receptor) (PTH/PTHr type I receptor).			
GN	Name=PTHr1; Synonyms=PTHr;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone;			
RX	MEDLINE=92212903; PubMed=1313566;			
RA	Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,			
RA	Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr.,			
RA	Kronenberg H.M., Segre G.V.;			
RT	"Expression cloning of a common receptor for parathyroid hormone and			
RT	parathyroid hormone-related peptide from rat osteoblast-like cells: a			
RT	single receptor stimulates intracellular accumulation of both cAMP and			
RL	inositol triphosphates and increases intracellular free calcium.";			
RN	Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992).			
RP	[2]			
RX	SEQUENCE FROM N.A.			
RA	MEDLINE=94292182; PubMed=8020952;			
RA	Pausova Z., Bourdon J., Clayton D., Mattei M.-G., Seldin M.F.,			
RA	Janicic N., Riviere M., Szpirer J., Levan G., Szpirer C.;			
RT	"Cloning of a parathyroid hormone/parathyroid hormone-related peptide			
RT	receptor (PTHr) cDNA from a rat osteosarcoma (UMR 106) cell line:			
RT	chromosomal assignment of the gene in the human, mouse, and rat			
RT	genomes.";			
RL	Genomics 20:20-26(1994).			
CC	-1- FUNCTION: This is a receptor for parathyroid hormone and for			
CC	parathyroid hormone-related peptide. The activity of this receptor			
CC	is mediated by g proteins which activate adenyl cyclase and also			
CC	a phosphatidylinositol-calcium second messenger system.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.			
CC	-----			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M77184; AAA41811.1; -			
DR	EMBL; L19475; AAA68098.1; -			
DR	PIR; I54195; I54195.			

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DR HSSP: Q03431; IBL1.
DR RGD; 3442; Pthrl.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
DR PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 26
FT CHAIN 27 591
FT
FT DOMAIN 27 188
FT TRANSMEM 189 212
FT DOMAIN 213 219
FT TRANSMEM 220 239
FT DOMAIN 240 282
FT TRANSMEM 283 306
FT DOMAIN 307 320
FT TRANSMEM 321 342
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FT TRANSMEM 362 382
FT DOMAIN 383 409
FT TRANSMEM 410 428
FT DOMAIN 429 440
FT TRANSMEM 441 463
FT DOMAIN 464 591
FT DISULFID 48 117
FT DISULFID 108 148
FT DISULFID 131 170
FT CARBOHYD 151 151
FT CARBOHYD 161 161
FT CARBOHYD 166 166
FT CARBOHYD 176 176
SQ SEQUENCE 591 AA; 66260 MW; 21944F3051B9E9C1 CRC64;
Query Match 95.8%; Score 2187; DB 1; Length 591;
Best Local Similarity 73.4%; Pred. No. 2.3e-156;
Matches 434; Conservative 0; Mismatches 1; Indels 156; Gaps 1;
Qy 1 MGAARIAPSLALLCCPVLSSAVAL----- 25
Db 1 MGAARIAPSLALLCCPVLSSAVALDADDVFTKEEQIFLLHRAQAQCKLKEVLHTAA 60
Qy 26 ----- 25
Db 61 NIMESDKGWTGTPASTGKPRKEKASGKFPYPSKENKENVPTGSRGRGRCPLPEWDNIVCWPL 120
Qy 26 ----- 25
Db 121 GAGEVAVPCPDYIDFNHKGHAYRCDRNGSWEVVPCHNRTWANYSECLKFWMTNETRE 180
Qy 26 -EVPDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNYYIHMHPLSPMLRAASIFVK 84
Db 181 REVFPDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNYYIHMHPLSPMLRAASIFVK 240
Qy 85 DAVLYSGFTIDEARLTDEELHIIAQVPPPPAAAGVACGRVATPFFLYFLATNYYWIL 144
Db 241 DAVLYSGFTIDEARLTDEELHIIAQVPPPPAAAGVACGRVATPFFLYFLATNYYWIL 300
Qy 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVGVGRATLANTCWDLSGCHK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLGPVAVFVAVGVGRATLANTCWDLSGCHK 360
Qy 205 WIQVPIIASVNLNFIILINIRVLATKLRETNAGRCDTTQQRKLLRSLVLVPLFGVH 264
Db 361 WIQVPIIASVNLNFIILINIRVLATKLRETNAGRCDTTQQRKLLRSLVLVPLFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILYFCFNGEVOAEIRKMSRWTLA 324
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Db 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSFGFFVAILYFCFNGEVOAEIRKMSRWTLA 480
Qy 325 LDFKFKARGSSSYSGPMVSHTSVTNVPAGLSLPLSPRLPPATNGHSQLPGHAKPG 384
Db 481 LDFKFKARGSSSYSGPMVSHTSVTNVPAGLSLPLSPRLPPATNGHSQLPGHAKPG 540
Qy 385 APATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 435
Db 541 APATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 591
RESULT 2
Q80WU8 PRELIMINARY; PRT; 591 AA.
ID Q80WU8
AC Q80WU8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Parathyroid hormone receptor 1.
GN Name=Pthrl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Splettenko M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BC051981; AAH51981.1; -.
DR HSSP; Q03431; IBL1.
DR MGD; MGI:97801; Pthrl.
DR GO; GO:0004991; P:parathyroid hormone receptor activity; TAS.
DR GO; GO:0030282; P:bone mineralization; IMP.
DR GO; GO:0001501; P:skeletal development; IMP.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR002170; Phrmn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00393; PTRHORMONER.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
KW Receptor.
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SQ SEQUENCE 591 AA; 66371 MW; C2E6C6AF2ABAFEEF CRC64;
Query Match 94.4%; Score 2156; DB 2; Length 591;
Best Local Similarity 72.4%; Pred. No. 5e-154;
Matches 428; Conservative 1; Mismatches 6; Indels 156; Gaps 1;

Qy 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGTARIAPSLALLCCPVLSAYALVDADDVFTKEQIFLLHRAQAQCDKLLKEVLHTAA 60
Qy 26 ----- 25
Db 61 NIMESDKGWTGTPASTSGKPRKEKAPKGYFPESENKENVPTGSRRRGRPCLPEDWNIWCPL 120
Qy 26 ----- 25
Db 121 GAGEVVAVPCPDYIYDFNHKGHAYRRCDNRNGSMEVVPVGHNRWTWANYSECLKFWNTRE 180
Qy 26 -EVFDRGLMIYTVGYSMSLASLTAVLILAYFRLHCTRNYYIHMHFSLFMLRAASIFVK 84
Db 181 REVDRLGLMIYTVGYSMSLASLTAVLILAYFRLHCTRNYYIHMHFSLFMLRAASIFVK 240
Qy 85 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVACRVAVTFFFLATNYYWIL 144
Db 241 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVACRVAVTFFFLATNYYWIL 300
Qy 145 VEGYLHSLIFMAFFSEKKYLGWTFIFGWLPAVFVAVVGVVATLANTCWDLSGHHK 204
Db 301 VEGYLHSLIFMAFFSEKKYLGWTFIFGWLPAVFVAVVGVVATLANTCWDLSGHHK 360
Qy 205 WIQVPIASVVLNFIINIRVATLKLRTNAGRCDTQQYRKLRSLTLVLVPLFGVH 264
Db 361 WIQVPIASVVLNFIINIRVATLKLRTNAGRCDTQQYRKLRSLTLVLVPLFGVH 420
Qy 265 YTVFMALPYTEVSGTLWQIQMHYEMLFNSQGFVAILIYFCNGEVOAEIRKSWRWTLA 324
Db 421 YTVFMALPYTEVSGTLWQIQMHYEMLFNSQGFVAILIYFCNGEVOAEIRKSWRWTLA 480
Qy 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSLPRLPATNTHGSQLPGHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSLPRLPATNTHGSQLPGHAKPG 540

RESULT 3
Q91WV4 ID Q91WV4 PRELIMINARY; PRT; 591 AA.
AC Q91WV4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Parathyroid hormone receptor 1.
GN Name=Pthr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Qy 385 APATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLQSGHWETVM 435
 Db 541 APAIENETIPVTMPKDDGFLNGSCGLDEASGSARPPPLQSGHWETVM 591

RESULT 5
 PTHR_HUMAN
 ID_PTHR_HUMAN STANDARD; PRT; 593 AA.
 AC Q03431;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE precursor (PTH/PTHrP receptor) (PTH/PTHrP type I receptor).
 GN Name=PTHr1; Synonyms=PTHr;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RC MEDLINE=93238641; PubMed=8386612; DOI=10.1210/en.132.5.2157;
 RA Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,
 RA Abou-Samra A.-B., Segre G.V., Jueppner H.;
 RT "Identical complementary deoxyribonucleic acids encode a human renal
 RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
 RL Endocrinology 132:2157-2165(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RC MEDLINE=93387403; PubMed=8397094; DOI=10.1016/0922-4106(93)90092-N;
 RA Schneider H., Feyen J.-H., Rao Movva N.;
 RT "Cloning and functional expression of a human parathyroid hormone
 RT receptor.";
 RL Eur. J. Pharmacol. 246:149-155(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95263723; PubMed=7745008; DOI=10.1210/jc.80.5.1611;
 RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,
 RA Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C.,
 RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,
 RA Abou-Samra A.-B., Segre G.V., Jueppner H.;
 RT "Pseudohypoparathyroidism type II is not caused by mutations in the
 RT coding exons of the human parathyroid hormone (PTH)/PTH-related
 RT peptide receptor gene.";
 RL J. Clin. Endocrinol. Metab. 80:1611-1621(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Levine M.A.;
 RT "Characterization of cDNA and genomic DNA encoding the human PTH/PTHrP
 RT receptor.";
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP EXTRACELLULAR DOMAIN DISULFIDE BONDS.
 RX MEDLINE=20374568; PubMed=10913300; DOI=10.1021/bi000142g;
 RA Grauschopf U., Lilie H., Honold K., Wozny M., Reusch D., Esswein A.,
 RA Schafer W., Rucknagel K.P., Rudolph R.;
 RT "The N-terminal fragment of human parathyroid hormone receptor 1
 RT constitutes a hormone binding domain and reveals a distinct disulfide
 RT pattern.";
 RL Biochemistry 39:8878-8887(2000).
 RN [6]
 RP STRUCTURE BY NMR OF 169-198.
 RX MEDLINE=96409426; PubMed=9737850; DOI=10.1021/bi981265h;
 RA Pellegrini M., Bisello A., Rosenblatt M., Chorev M., Mierke D.F.;
 RT "Binding domain of human parathyroid hormone receptor: from
 RT conformation to function.";
 RL Biochemistry 37:12737-12743(1998).
 RN [7]
 RP VARIANT JMC ARG-223.
 RX MEDLINE=95215874; PubMed=7701349;

RA Schipani E., Kruse K., Jueppner H.;
 RT "A constitutively active mutant PTH-PTHrP receptor in Jansen-type
 RT metaphyseal chondrodysplasia.";
 RL Science 268:98-100(1995).
 RN [8]
 RP VARIANTS JMC ARG-223 AND PRO-410.
 RX MEDLINE=96366745; PubMed=8703170; DOI=10.1056/NEJM199609053351004;
 RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
 RA Kooh S.W., Cole W.G., Jueppner H.;
 RT "Constitutively activated receptors for parathyroid hormone and
 RT parathyroid hormone-related peptide in Jansen's metaphyseal
 RT chondrodysplasia.";
 RL N. Engl. J. Med. 335:708-714(1996).
 RN [9]
 RP CHARACTERIZATION OF VARIANTS JMC ARG-223 AND PRO-410.
 RX MEDLINE=97322091; PubMed=9178745; DOI=10.1210/me.11.7.851;
 RA Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,
 RA Jueppner H.;
 RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate
 RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide
 RT receptors mutated at the two loci for Jansen's metaphyseal
 RT chondrodysplasia.";
 RL Mol. Endocrinol. 11:851-858(1997).
 RN [10]
 RP VARIANT BOD LEU-132.
 RX MEDLINE=98417978; PubMed=9745456; DOI=10.1210/jc.83.9.3373;
 RA Zhang P., Jobert A.-S., Couvineau A., Silve C.;
 RT "A homozygous inactivating mutation in the parathyroid
 RT hormone/parathyroid hormone-related peptide receptor causing
 RT Blomstrand chondrodysplasia.";
 RL J. Clin. Endocrinol. Metab. 83:3365-3368(1998).
 RN [11]
 RP VARIANT JMC ARG-458.
 RX MEDLINE=99415605; PubMed=10487664; DOI=10.1210/jc.84.9.3052;
 RA Schipani E., Langman C.B., Hunzelman J., Le Merrer M., Loke K.Y.,
 RA Dillon M.J., Silve C., Jueppner H.;
 RT "A novel parathyroid hormone (PTH)/PTH-related peptide receptor
 RT mutation in Jansen's metaphyseal chondrodysplasia.";
 RL J. Clin. Endocrinol. Metab. 84:3052-3057(1999).
 RN [12]
 RP VARIANT ENCHONDROMATOSIS CVS-150.
 RX MEDLINE=21918585; PubMed=11850620; DOI=10.1038/ng844;
 RA Hopyan S., Gokgoz N., Poon R., Gensure R.C., Yu C., Cole W.G.,
 RA Bell R.S., Jueppner H., Andrulis I.L., Wunder J.S., Alman B.A.;
 RT "A mutant PTH/PTHrP type I receptor in enchondromatosis.";
 RL Nat. Genet. 30:306-310(2002).
 CC -I- FUNCTION: This is a receptor for parathyroid hormone and for
 CC parathyroid hormone-related peptide. The activity of this receptor
 CC is mediated by g proteins which activate adenylyl cyclase and also
 CC a phosphatidylinositol-calcium second messenger system.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- TISSUE SPECIFICITY: Expressed in most tissues. Most abundant in
 CC kidney, bone and liver.
 CC -I- DISEASE: Defects in PTHr1 are the cause of Jansen's metaphyseal
 CC chondrodysplasia (JMC) [MIM:156400]. JMC is a rare autosomal
 CC dominant disorder characterized by a short-limbed dwarfism
 CC associated with hypercalcemia and normal or low serum
 CC concentrations of the two parathyroid hormones.
 CC -I- DISEASE: Defects in PTHr1 are the cause of chondrodysplasia
 CC Blomstrand type (BOCD) [MIM:215045]. BOCD is a severe skeletal
 CC dysplasia.
 CC -I- DISEASE: Defects in PTHr1 can be a cause of enchondromatosis
 CC [MIM:166000]. Enchondromas are common benign cartilage tumors of
 CC bone. They can occur as solitary lesions or as multiple lesions in
 CC enchondromatosis (Ollier and Maffucci diseases). Clinical problems
 CC caused by enchondromas include skeletal deformity and the
 CC potential for malignant change to osteosarcoma.
 CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
 CC -----
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 CC -----

DR EMBL; L04308; AAA36525.1; -;
 DR EMBL; L68596; CAA48589.1; -;
 DR EMBL; U22409; AAB60657.1; -;
 DR EMBL; U22401; AAB60657.1; JOINED.
 DR EMBL; U22402; AAB60657.1; JOINED.
 DR EMBL; U22403; AAB60657.1; JOINED.
 DR EMBL; U22404; AAB60657.1; JOINED.
 DR EMBL; U22405; AAB60657.1; JOINED.
 DR EMBL; U22406; AAB60657.1; JOINED.
 DR EMBL; U22407; AAB60657.1; JOINED.
 DR EMBL; U22408; AAB60657.1; JOINED.
 DR EMBL; U17418; AAA56774.1; -;
 DR PIR; I38139; A49191.
 DR PDB; 1BLJ; NMR; @=168-198.
 DR PDB; 1ET2; Model; S=168-469.
 DR PDB; 1ET3; Model; S=168-469.
 DR Genew; HGNC:9608; PTHR1.
 DR MIM; 168468; -;
 DR MIM; 156400; -;
 DR MIM; 215045; -;
 DR MIM; 166000; -;
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0004991; F:parathyroid hormone receptor activity; TAS.
 DR GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.
 DR GO; GO:0001501; P:skeletal development; TAS.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
 DR 3D-structure; Disease mutation; Dwarfism; G-protein coupled receptor;
 KW Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 593 Parathyroid hormone/parathyroid hormone-
 related peptide receptor.
 FT DOMAIN 27 188 Extracellular (Potential).
 FT TRANSMEM 189 212 1 (Potential).
 FT DOMAIN 213 219 Cytoplasmic (Potential).
 FT TRANSMEM 220 239 2 (Potential).
 FT DOMAIN 240 282 Extracellular (Potential).
 FT TRANSMEM 283 306 3 (Potential).
 FT DOMAIN 307 320 Cytoplasmic (Potential).
 FT TRANSMEM 321 342 4 (Potential).
 FT DOMAIN 343 361 Extracellular (Potential).
 FT TRANSMEM 362 382 5 (Potential).
 FT DOMAIN 383 409 Cytoplasmic (Potential).
 FT TRANSMEM 410 428 6 (Potential).
 FT DOMAIN 429 440 Extracellular (Potential).
 FT TRANSMEM 441 463 7 (Potential).
 FT DOMAIN 464 593 Cytoplasmic (Potential).

Query Match 88.0%; Score 2008; DB 1; Length 593;
 Best Local Similarity 67.3%; Pred. No. 7.1e-143;
 Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

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Db 1 MGTARIAPGLALLCCPVLSSAYALVDVDDVMTKEEQIFLLHRAQAQCKELKEVLORPA 60

QY 26 ----- 25

Db 61 SIMESDKGWTASSTSGKPRDKASGLYPSEDEKAPTGSRYGRPCLPWDHILCWPL 120

QY 26 ----- 25
 Db 121 GAGEVAVPCDDYIYDFNHKGHAYRRCDRNGSWELVPGHNRWTWYSECVKLTNETRE 180
 QY 26 -EVFDRLGMIYTVGYSGMSLASLTVAVLILAYFRRLHCTRNYIHHMFLSFMLRAASIFVK 84
 Db 181 REVFDRLGMIYTVGYSVSLASLTVAVLILAYFRRLHCTRNYIHHMFLSFMLRAVSIK 240
 QY 85 DAVLYSGFTLDEAERLTELHIIAQVPPPPAAAAGYAGCRVAVTFFLYFLATNYWIL 144
 Db 241 DAVLYSGATLDEAERLTELHIIAQVPPPPAAAAGYAGCRVAVTFFLYFLATNYWIL 300
 QY 145 VEGLYLHSLIFMAFFSEKKYLGWGTTFGWLPLPAVFVAVMVGVVRATLANTCWDLSSGKK 204
 Db 301 VEGLYLHSLIFMAFFSEKKYLGWGTTFGWLPLPAVFVAVMVGVVRATLANTCWDLSSGKK 360
 QY 205 WIIQVPIASVILNFILFINIRVLATKLRETNAGRCDTQQYRKLRLSTLVLPLFGVH 264
 Db 361 WIIQVPIASVILNFILFINIRVLATKLRETNAGRCDTQQYRKLRLSTLVLPLFGVH 420
 QY 265 YTVFMALPYTEVSGTLWQIMHYEMLFNSFGQFFVAILIYFCNGEVOAEIKKSWSRWTLA 324
 Db 421 YIVFMATPYTEVSGTLWQIMHYEMLFNSFGQFFVAILIYFCNGEVOAEIKKSWSRWTLA 480
 QY 325 LDFKRRKARGSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATTNGHSOLPGHAKP 383
 Db 481 LDFKRRKARGSSSYSGPMVSHTSVTNVGPRVGLGLPLSPRLLPTATTNGHPOLPGHAKP 540
 QY 384 GAPATET-ETLPVTMAVPKDDGFLNGSCGLDEASGSRAPPLLOQMETVM 435
 Db 541 GTPALETLETTTPMAAAPKDDGFLNGSCGLDEASGSRAPPLLOQMETVM 593

RESULT 6

Q9TU31 PRELIMINARY; PRT; 595 AA.
 ID O9TU31
 AC O9TU31;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Parathyroid hormone receptor-1.
 GN Name=PTH1;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RC TISSUE=Kidney;
 RA Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF167095; AAD55938.1; -;
 DR HSSP; Q03431; 1BL1.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
 DR GO; GO:0004931; F:parathyroid hormone receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR InterPro; IPR002170; Phrmn_receptor.
 DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; PR00393; PTHRMONER.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
 KW Receptor.
 SQ SEQUENCE 595 AA; 66308 MW; 09568ECF38D4D258 CRC64;

Query Match 85.7%; Score 1957; DB 2; Length 595;
 Best Local Similarity 65.6%; Pred. No. 4.9e-139;
 Matches 394; Conservative 11; Mismatches 24; Indels 172; Gaps 5;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
 DB 1 MGAARIAPSLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCKRLKEVLQRP 60
 QY 26 ----- 25
 DB 61 DIMESDKGWSASTSGPKKKEKAGSLYPESEEDKEVPTGSRHRGRPCLPEDWHILCWPL 120
 QY 26 ----- 25
 DB 121 GAGEVAVPCPDYIYDFNHKGHAYRRCDRNGSMELVPGHNRWTANYSECVKELTNETRE 180
 QY 26 -EVPDRGLMIYTVGYSMASLASLTAVLILAYFRRLHCTRYNIHMHPLSLMRAASIFVK 84
 DB 181 REVFDRLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRYNIHMHPLSLMRAVSIFVK 240
 QY 85 DAVLYSGFTLDEARLTTEBELHIIAQVPPPPAAAAGYACRVAVTFFLYFLATNYWIL 144
 DB 241 DAVLYSGATLDEARLTTEBELRAIAQAAPPPTAAA-GYAGCRVAVTFFLYFLATNYWIL 299
 QY 145 VEGLYLHSLIFMAFFSEKKYLGWTFIFGWLPAVFVAVVGVVRATLANTCGDLSGHHK 204
 DB 300 VEGLYLHSLIFMAFFSEKKYLGWTFIFGWLPAVFVAVVGVVRATLANTCGDLSGHHK 359
 QY 205 WIIQVPIASVNLFLFINIRVLATKLRNAGRCRTQQRKLLRSTLVLPVFGVH 264
 DB 360 WIIQVPIASVNLFLFINIRVLATKLRNAGRCRTQQRKLLRSTLVLPVFGVH 419
 QY 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA 324
 DB 420 YIVFMATPYTEVSGTLWQIOMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA 479
 QY 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPP-----ATTNGHSOL 377
 DB 480 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPAAAAATTATTNGHPPI 539
 QY 378 PGHAKGAPATETETLPVT---NAVPKDGDGFLNGSCGLDEEASGAPRPPALLOEWETV 434
 DB 540 PGHTKGPAP-----TLPATPPATAAPKDDGFLNGSCGLDEEASAPERPPALLOEWETV 594
 QY 435 M 435
 DB 595 M 595

RESULT 7
 Q7YRI3 PRELIMINARY; PRT; 599 AA.
 AC Q7YRI3
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone related protein receptor.
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 OC Cervinae; Cervus.
 OC NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu H., Barling P.M., Ma L., Nicholson L.F.B.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AY328401; AAP93208.1;
 DR HSSP; Q03431; 1BL1.
 DR GO; GO:0016020; C-membrane; IEA.
 DR GO; GO:0004930; F-G-protein coupled receptor activity; IEA.
 DR GO; GO:0004872; F-receptor activity; IEA.
 DR InterPro; IPR000832; GPCR secretin.
 DR DR InterPro; IPR001879; hormn_receptor.

DR Pfam; PF00002; 7tm_2; 1.
 DR Pfam; PF02793; HRM; 1.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G PROTEIN RECP F2_1; 1.
 DR PROSITE; PS0227; G PROTEIN RECP F2_3; 1.
 DR PROSITE; PS0261; G-PROTEIN RECP F2_4; 1.
 KW Receptor.
 SQ SEQUENCE. 589 AA; 65733 MW; 08A0577FB042A77A CRC64;

Query Match 84.6%; Score 1932; DB 2; Length 589;
 Best Local Similarity 65.2%; Pred. No. 3.7e-137;
 Matches 386; Conservative 15; Mismatches 31; Indels 160; Gaps 4;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
 DB 1 MGAARIAPSLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCKRLKEVLQRP 60
 QY 26 ----- 25
 DB 61 DIMESDKGWSASTSGPKKKEKAGSLYPESEEDKEVPTGSRPRGRPCLPEDWHILCWPM 120
 QY 26 ----- 25
 DB 121 GAGEVAVPCPDYIYDFNHKGHAYRRCDRNGSMELVPGHNRWTANYSECVKELTNETRE 180
 QY 26 -EVPDRGLMIYTVGYSMASLASLTAVLILAYFRRLHCTRYNIHMHPLSLMRAASIFVK 84
 DB 181 REVFDRLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRYNIHMHPLSLMRAVSIFVK 240
 QY 85 DAVLYSGFTLDEARLTTEBELHIIAQVPPPPAAAAGYACRVAVTFFLYFLATNYWIL 144
 DB 241 DAVLYSGATLDEARLTTEBELRAIAQAAPPPTAAA-GYVGRVAVTFFLYFLATNYWIL 299
 QY 145 VEGLYLHSLIFMAFFSEKKYLGWTFIFGWLPAVFVAVVGVVRATLANTCGDLSGHHK 204
 DB 300 VEGLYLHSLIFMAFFSEKKYLGWTFIFGWLPAVFVAVVGVVRATLANTCGDLSGHHK 359
 QY 205 WIIQVPIASVNLFLFINIRVLATKLRNAGRCRTQQRKLLRSTLVLPVFGVH 264
 DB 360 WIIQVPIASVNLFLFINIRVLATKLRNAGRCRTQQRKLLRSTLVLPVFGVH 419
 QY 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA 324
 DB 420 YIVFMATPYTEVSGTLWQIOMHYEMLFNSFGFFGAILIYFCNGEVOAEIRKSWRWTLA 479
 QY 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPP-----LPPATTNGHSOLPGHAKP 383
 DB 480 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRGLPLSPRLPPATTNGHPPPLPGHTKS 539
 QY 384 GAPATETETLPVTMAVPKDDGFLNGSCGLDEEASGAPRPPALLOEWETVM 435
 DB 540 GSPA--LQATPPAATAAPKDDGFLNGSCGLDEEACAPERPPVLLQEWETVM 589

RESULT 8
 PTHR_PIG STANDARD; PRT; 585 AA.
 AC P50133;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE precursor (PTH/PTHr receptor) (PTH/PTHr type I receptor).
 GN Name=PTHRI; Synonyms=PTHr;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96305358; PubMed=8688470; DOI=10.1016/0167-4781(96)00035-8;
 RA Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,
 RA Chandrasekhar S., Hsiung H.M.;

RT "Structure and functional expression of a complementary DNA for
 RT porcine parathyroid hormone/parathyroid hormone-related peptide
 RL receptor";
 RL Biochim. Biophys. Acta 1307:339-347(1996).
 CC -1- FUNCTION: This is a receptor for parathyroid hormone and for
 CC parathyroid hormone-related peptide. The activity of this receptor
 CC is mediated by G proteins which activate adenylyl cyclase and also
 CC a phosphatidylinositol-calcium second messenger system (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
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 CC -----
 DR EMBL; U18315; AAC48619.1; -;
 DR HSSP; Q03431; IBL1.
 DR InterPro; IPR000832; GPCR secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR Pfam; PF00002; 7tm.2; 1.
 DR Pfam; PF02793; HRM1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR SMART; SM00008; Hormr; 1.
 DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
 DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
 DR PROSITE; PS00261; G_PROTEIN_RECP_F2_4; 1.
 KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 26
 FT CHAIN 27 585
 FT FT
 FT DOMAIN 27 184
 FT TRANSFEM 185 208
 FT DOMAIN 209 215
 FT TRANSFEM 216 235
 FT DOMAIN 236 277
 FT TRANSFEM 278 301
 FT DOMAIN 302 315
 FT TRANSFEM 316 337
 FT DOMAIN 338 356
 FT TRANSFEM 357 377
 FT DOMAIN 378 404
 FT TRANSFEM 405 423
 FT DOMAIN 424 435
 FT TRANSFEM 436 458
 FT DOMAIN 459 585
 FT DISULFID 48 113
 FT DISULFID 104 144
 FT DISULFID 127 166
 FT CARBOHYD 147 157
 FT CARBOHYD 157 172
 FT CARBOHYD 162 172
 FT CARBOHYD 172 172
 SQ SEQUENCE 585 AA; 65682 MW; 60BE15CD49B7D210 CRC64;
 Query Match 84.3%; Score 1925; DB 1; Length 585;
 Best Local Similarity 65.6%; Pred. No. 1.2e-136;
 Matches 386; Conservative 13; Mismatches 33; Indels 156; Gaps 4;
 Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
 Db 1 MGAARIAPGLALLCCPVLSSAYALVDDVMTKEQIFLLHRAQAQCKRLKEVLQRP 60
 Qy 26 ----- 25
 Db 61 DIMESDKGWSAAPTSGKPRKEKAGSKLYPESGDTGSRHQRCPLPEWDHLCWPLGAPG 120
 Qy 26 -----EVF 28

Db 121 EVVAMPCPDYIDFNHKGHAYRRCDRNGSWELVPGHNRTWANYSECVKFLTNETREVEF 180
 Qy 29 DRIGMTYTVGYSMSLASLTVAVLILAYFRRLHCTRYIHHMFSLPMLRAASIFVKDAVL 88
 Db 181 DRIGMTYTVGYSMSLASLTVAVLILAYFRRLHCTRYIHHMFSLPMLRAASIFVKDAVL 240
 Qy 89 YSGFTLDEAERLTERELHIIAQVPPPPAAAAGVACRVAVTFFLYFLATNYWILVEGL 148
 Db 241 YSGATLDEAERLTERELHIIAQVPPPPAAAAGVACRVAVTFFLYFLATNYWILVEGL 239
 Qy 149 YLHSLIFMAFFSEKYLWGTTFGWLGPVAVVAVVGVVGRATLANTCWLSSGKKWIIQ 208
 Db 300 YLHSLIFMAFFSEKYLWGTTFGWLGPVAVVAVVGVVGRATLANTCWLSSGKKWIIQ 359
 Qy 209 VPIASVVLNFIINIRVLATKLRETNAGRCDTQOYKRLRLTLVLPFGVHYTVF 268
 Db 360 VPIASVVLNFIINIRVLATKLRETNAGRCDTQOYKRLRLTLVLPFGVHYTVF 419
 Qy 269 MALPYTEVSTLWQIQMHYEMLFNSFGPFVAILIYFCNGEVOAEIKRWSRWTLALDFK 328
 Db 420 MATPYTEVSTLWQIQMHYEMLFNSFGPFVAILIYFCNGEVOAEIKRWSRWTLALDFK 479
 Qy 329 RKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATNGHSQLPGHAKGPAA 387
 Db 480 RKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPR-LPPATNGHSQLPGHAKGPAA 539
 Qy 388 TETETLPTVMVAPKDDGFLNGSCGDLDEASGASRPPILQEGWETVM 435
 Db 540 --LQTTTPVVAAPKDDGFLNGSCGDLDEASGASRPPILQEGWETVM 585
 RESULT 9
 PTHR_DIDMA STANDARD; PRT; 585 AA.
 AC P25107;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor
 DE Precursor (PTH/PTHrP receptor) (PTH/PTHrP type I receptor).
 GN Names=PTHr1; Synonyms=PTHr;
 OS Didelphis marsupialis virginiana (North American opossum).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
 OX NCBI_TaxID=9267;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92054592; PubMed=1658941;
 RA Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-F., Schipani E.,
 RA Richards J., Kolakowski L.F. Jr., Hock J., Potts J.T. Jr.,
 RA Kronenberg H.M., Segre G.V.;
 RT "A G protein-linked receptor for parathyroid hormone and parathyroid
 RT hormone-related peptide";
 RL Science 254:1024-1026(1991).
 CC -1- FUNCTION: This is a receptor for parathyroid hormone and for
 CC parathyroid hormone-related peptide. The activity of this receptor
 CC is mediated by G proteins which activate adenylyl cyclase and also
 CC a phosphatidylinositol-calcium second messenger system.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M74445; AAA30979.1; -;
 DR FIR; A39286; A39286.
 DR HSSP; Q03431; IBL1.

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OM protein - protein search, using sw model

Run on: July 4, 2005, 06:12:59 ; Search time 84 Seconds
(without alignments)
2002.866 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 435

Sequence: 1 MGARIAPSLALLCCPVLS.....EASGSARPPPLQGHWTVM 435

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	100.0	435	3 AAB07529	Aab07529 A mutant
2	410	94.3	446	3 AAY96983	Aay96983 Tethered
3	410	94.3	591	2 AAR92277	Aar92277 Rat bone
4	410	94.3	591	2 AAW73316	Aaw73316 Parathyro
5	410	94.3	591	8 ADH61247	Adh61247 Rat bone
6	404	92.9	591	7 ADE83416	Ade83416 Rat Prote
7	324	74.5	324	3 AAY96985	Aay96985 Tethered
8	318	73.1	591	8 ADO29629	Ado29629 Mouse GPC
9	309	71.0	591	2 AAR27706	Aar27706 Rat bone
10	299	68.7	335	3 AAY96984	Aay96984 Tethered
11	49	11.3	435	3 AAY96987	Aay96987 Human tet
12	49	11.3	448	3 AAY96986	Aay96986 Human tet
13	49	11.3	450	3 AAY96988	Aay96988 Human tet
14	49	11.3	593	2 AAW73317	Aaw73317 Human par
15	49	11.3	593	4 ABB56385	Abb56385 Non-endog
16	49	11.3	593	4 AAB71876	Aab71876 Human PTR
17	49	11.3	593	6 ABP81872	Abp81872 Human par
18	49	11.3	593	7 ADE83418	Ade83418 Human pro
19	49	11.3	593	7 ADF70390	Adf70390 Human PTH
20	49	11.3	593	8 ADH61248	Adh61248 Human PTH
21	49	11.3	593	8 ADO29628	Ado29628 Human GPC
22	49	11.3	593	8 ADO18189	Ado18189 Human sof
23	49	11.3	593	8 ADQ76825	Adq76825 Human wil
24	49	11.3	593	8 ADR47544	Adr47544 Human par
25	49	11.3	595	6 ABG73825	Abg73825 Canine pa

26	49	11.3	614	2 AAR27707	Aar27707 Human kid
27	49	11.3	975	8 ADQ76835	Adq76835 Parathyro
28	43	9.9	964	7 ADC86169	Adc86169 Human GPC
29	40	9.2	129	8 ADQ76849	Adq76849 Human par
30	40	9.2	289	8 ADQ76854	Adq76854 Parathyro
31	40	9.2	325	8 ADQ76855	Adq76855 Parathyro
32	40	9.2	339	8 ADQ76856	Adq76856 Parathyro
33	40	9.2	354	8 ADQ76857	Adq76857 Parathyro
34	40	9.2	368	8 ADQ76858	Adq76858 Parathyro
35	34	7.8	34	6 ABR61989	AbR61989 Human par
36	34	7.8	515	2 AAR27704	Aar27704 Opossum k
37	34	7.8	515	2 AAR92275	Aar92275 Opossum k
38	34	7.8	515	2 AAW73314	Aaw73314 Parathyro
39	34	7.8	515	8 ADH61245	Adh61245 Opossum k
40	34	7.8	585	2 AAR27705	Aar27705 Opossum k
41	34	7.8	585	2 AAR92276	Aar92276 Opossum k
42	34	7.8	585	2 AAW73315	Aaw73315 Parathyro
43	34	7.8	585	8 ADH61246	Adh61246 Opossum k
44	31	7.1	593	2 AAR92278	Aar92278 Human kid
45	29	6.7	275	8 ADQ76853	Adq76853 Parathyro

ALIGNMENTS

RESULT 1
AAB07529
ID AAB07529 standard; protein; 435 AA.
XX
AC AAB07529;
XX
DT 20-OCT-2000 (first entry)
XX
DE A mutant parathyroid hormone (PTH) receptor designated rdeltaNt.
XX
KW Mutant; parathyroid hormone; PTH; receptor; rdeltaNt;
KW ligand binding domain.
XX
OS Homo sapiens.
XX
PH Key
FT Peptide
FT Protein
FT Protein
FT Protein
PN WO200040698-A1.
XX
PD 13-JUL-2000.
XX
PF 31-DEC-1998; 98WO-US027862.
XX
PR 31-DEC-1998; 98WO-US027862.
XX
PA (GENO) GEN HOSPITAL CORP.
XX
PI Gardella TJ, Kronenberg HM, Potts JT;
XX
DR WPI; 2000-465971/40.
DR N-PSDB; AAS58932.
XX
PT New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a deletion of the extracellular amino-terminus ligand binding domain, useful in screening assays for identifying agonists and antagonists of PTH receptor activity.
XX
PS Claim 17; Fig 1; 81pp; English.
XX
CC The present sequence represents a mutant parathyroid hormone (PTH) receptor, designated rdeltaNt. The polypeptide is characterized by a deletion of the extracellular amino-terminus ligand binding domain. The receptor has a minimal domain for ligand binding and is, therefore, useful in screening assays designed for the identification of agonists

CC	and antagonists of PTH receptor activity
XX	
SQ	Sequence 435 AA;
	Query Match 100.0%; Score 435; DB 3; Length 435;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MGARAPSLALLCCPVLSSAYALEVDFRLGMIYTVGYSMASLSTAVAILLAYFRRLH 60
DB	1 MGARAPSLALLCCPVLSSAYALEVDFRLGMIYTVGYSMASLSTAVAILLAYFRRLH 60
QY	61 CTRNYIHMFSLFMLRAASIFVKDAVLYSGFTLDEAERLTETEEELHHIAQVPPPPAAA 120
DB	61 CTRNYIHMFSLFMLRAASIFVKDAVLYSGFTLDEAERLTETEEELHHIAQVPPPPAAA 120
QY	121 GYAGCRVATFFLYFLATNYYILVEGLYLHSLIFMAFFSEKKYLWGTFIFGWGLPAVF 180
DB	121 GYAGCRVATFFLYFLATNYYILVEGLYLHSLIFMAFFSEKKYLWGTFIFGWGLPAVF 180
QY	181 AVWVGVRATLANTGCWDLSGGHKMIIQVPILASVVLNFILFINIRVLATKLRETNAGR 240
DB	181 AVWVGVRATLANTGCWDLSGGHKMIIQVPILASVVLNFILFINIRVLATKLRETNAGR 240
QY	241 CDTRQQRKLLRSTLVLPFGVHYTVFMALPYTEVSGTLQIQMHYEMLFNSFGGFVA 300
DB	241 CDTRQQRKLLRSTLVLPFGVHYTVFMALPYTEVSGTLQIQMHYEMLFNSFGGFVA 300
QY	301 IIVCFNGEVOAEIRKSWSRWTLALDPFKKARSQSSSYSGPMVSHTSVTVNGPRAGLSL 360
DB	301 IIVCFNGEVOAEIRKSWSRWTLALDPFKKARSQSSSYSGPMVSHTSVTVNGPRAGLSL 360
QY	361 PLSPRPPTATTNGHSOLPGHAKPGAPATETPLVTMAVPKDDGFLNGSCSGLDEBASGS 420
DB	361 PLSPRPPTATTNGHSOLPGHAKPGAPATETPLVTMAVPKDDGFLNGSCSGLDEBASGS 420
QY	421 ARPPPLLQEGWETVM 435
DB	421 ARPPPLLQEGWETVM 435
RESULT 2	AAY96983 standard; protein; 446 AA.
ID	
AC	AAY96983;
XX	
DT	31-OCT-2000 (first entry)
XX	Tethered PTH-1 receptor, Tetherl.
DE	
XX	PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW	PTH-1 receptor; resorption; remodeling; tetherl.; osteoporosis.
OS	Rattus sp.
OS	Synthetic.
OS	Chimeric.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..23 /label= PTH-1_receptor_signal_sequence
FT	Peptide 24..32 /label= PTH_residues_1-9
FT	Peptide 33..36 /label= linker
FT	Protein 37..446 /label= PTH-1_receptor
FT	/note= "residue 182 to end"
XX	
PX	WO200039278-A2.
XX	
PD	06-JUL-2000.
XX	

XX AC AAR92277;
XX 25-MAR-2003 (revised)
DT 18-MAY-1996 (first entry)
XX
XX DE Rat bone PTH/PTHrP receptor.
XX
XX Parathyroid hormone; receptor; parathormone; PTH;
KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
KW hypercalcaemia; hypocalcaemia; cancer.
XX
XX Rattus sp.
XX
XX Key Location/Qualifiers
FH 1. .192
FT /label= Extracellular_region
FT 193. .211
FT /label= Transmembrane_region
FT 212. .221
FT /label= Intracellular_region
FT 222. .240
FT /label= Transmembrane_region
FT 241. .299
FT /label= Extracellular_region
FT 300. .316
FT /label= Transmembrane_region
FT 317. .325
FT /label= Intracellular_region
FT 326. .342
FT /label= Transmembrane_region
FT 343. .364
FT /label= Extracellular_region
FT 365. .383
FT /label= Transmembrane_region
FT 384. .408
FT /label= Intracellular_region
FT 409. .428
FT /label= Transmembrane_region
FT 429. .444
FT /label= Intracellular_region
FT 445. .463
FT /label= Transmembrane_region
FT 464. .591
FT /label= Intracellular_region
XX US5494806-A.
XX 27-FEB-1996.
XX
XX 06-APR-1992; 92US-00864475.
XX
XX 05-APR-1991; 91US-00681702.
XX (GEO) GEN HOSPITAL CORP.
XX Potts JT, Juppner H, Segre GV, Schipani E, Kronenberg HM;
PI Abou-Samra A;
XX WPI; 1996-139028/14.
DR N-PSDB; AAT15947.
XX
XX DNA encoding vertebrate parathyroid hormone receptor - useful for
PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia, cancer
PT etc.
XX
XX Claim 1; Fig 3A-3E; 64pp; English.
XX
XX A rat parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
CC receptor (AAR92277) is encoded by cDNA clone R15B (AAT15947) isolated
CC from a rat osteosarcoma ROS 17/2.8 CDNA library. The receptor a G-protein
CC linked receptor having 7 transmembrane domains. It induces an increase in
CC intracellular cAMP and calcium upon challenge with PTH or PTHrP.

CC Recombinant receptor can be produced in vector/host cell systems and used
CC in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and
CC hypocalcaemia, to screen for (ant)agonists and to raise antibodies. Host
CC cells expressing the receptor are used for diagnostic measurement of PTH
CC serum levels. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 591 AA;
XX
XX Query Match 94.3%; Score 410; DB 2; Length 591;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 26 EYEDRLGMIYTCYSNLSASLTAVNLILAYFRRLHCTRNIIHMHMFLSEFLRAASIFVKD 85
XX DB 182 EYEDRLGMIYTCYSNLSASLTAVNLILAYFRRLHCTRNIIHMHMFLSEFLRAASIFVKD 241
XX QY 86 AVLYSGFTLDEAERLLEEELHIIAQVPPPPAAAAGVAGCRVAVTFPLFLATNYWILV 145
XX DB 242 AVLYSGFTLDEAERLLEEELHIIAQVPPPPAAAAGVAGCRVAVTFPLFLATNYWILV 301
XX QY 146 EGYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFVAWVGVRATLANTGCWDLSSGHKKW 205
XX DB 302 EGYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFVAWVGVRATLANTGCWDLSSGHKKW 361
XX QY 206 IIQVPILASVVLNFIILFINIRVLATKLRETNAGRCOTRQYRKLRLSTLVLVPLFGVHY 265
XX DB 362 IIQVPILASVVLNFIILFINIRVLATKLRETNAGRCOTRQYRKLRLSTLVLVPLFGVHY 421
XX QY 266 TVFMALPYTEVSGTLWQIOHMYEMLFNSFGQFPFVAILIYFCNGEVOAEIRKRSRWTLAL 325
XX DB 422 TVFMALPYTEVSGTLWQIOHMYEMLFNSFGQFPFVAILIYFCNGEVOAEIRKRSRWTLAL 481
XX QY 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPCHAKPGA 385
XX DB 482 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPCHAKPGA 541
XX QY 386 PATETETLPTWMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGHWETVM 435
XX DB 542 PATETETLPTWMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGHWETVM 591
XX
XX RESULT 4
XX AAW73316
XX ID AAW73316 standard; protein; 591 AA.
XX AC AAW73316;
XX DT 08-FEB-1999 (first entry)
XX DE Parathyroid hormone receptor R15B.
XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
XX KW PTH-related hypercalcaemia; rat.
XX OS Rattus sp.
XX US5840853-A.
XX 24-NOV-1998.
XX 06-JUN-1995; 95US-00471494.
XX 05-APR-1991; 91US-00681702.
XX 06-APR-1992; 92US-00864475.
XX (GEO) GEN HOSPITAL CORP.
XX Abou-Samra A, Juppner H, Potts JT, Segre GV, Schipani E;
XX Kronenberg HM;
XX WPI; 1999-034124/03.
XX N-PSDB; AAV08390.

PT Antibody to parathyroid hormone receptor - for diagnostic or therapeutic use.

XX Claim 6; Fig 3; 63pp; English.

CC This sequence represents the rat parathyroid hormone (PTH) receptor R15B, which is targeted by the antibody of the invention. The antibody of the invention is immunoreactive with naturally occurring human, rat or opossum PTH receptor. The antibody is useful for treating disorders characterised by overstimulation of PTH receptors by their ligand and for the diagnosis of PTH-related hypercalcaemia

XX Sequence 591 AA;

Query Match 94.3%; Score 410; DB 2; Length 591;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EVFDRLGMIYTVGYSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVKD 85
 DB 182 EVFDRLGMIYTVGYSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVKD 241

QY 86 AVLYSGFTLDEAERLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYWILV 145
 DB 242 AVLYSGFTLDEAERLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYWILV 301

QY 146 EGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVWVGVATLANTGCDLSSGHKKW 205
 DB 302 EGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVWVGVATLANTGCDLSSGHKKW 361

QY 206 IIOVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVHY 265
 DB 362 IIOVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVHY 421

QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAIYFCNGEVSQAEIRKSNRWTLAL 325
 DB 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAIYFCNGEVSQAEIRKSNRWTLAL 481

QY 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSRPLPATTTNGHSQLPCHAKPGA 385
 DB 482 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSRPLPATTTNGHSQLPCHAKPGA 541

QY 386 PATETETLPVTMAVPKDDGFLNGSCGLDEASGSRPPPLQGGWETVM 435
 DB 542 PATETETLPVTMAVPKDDGFLNGSCGLDEASGSRPPPLQGGWETVM 591

RESULT 5
 ADH61247
 ID ADH61247 standard; protein; 591 AA.
 XX AC ADH61247;
 XX DT 25-MAR-2004 (first entry)
 XX DE Rat bone PTH/PTHrP receptor, R15B.
 XX KW osteopathic; Parathyroid hormone receptor; hypercalcaemia;
 XX KW hyperparathyroidism; osteoporosis; carcinoma; epidermoid cancer;
 KW oesophagus multiple myeloma; hypocalcaemia; cytostatic; rat; PTH; PTHrP;
 KW PTH-related protein; receptor.
 XX OS Rattus rattus.
 XX FH Key
 FT Region 193..211
 FT /note= "Transmembrane region 1"
 FT Region 222..240
 FT /note= "Transmembrane region 2"
 FT Region 300..316
 FT /note= "Transmembrane region 3"
 FT Region 326..342
 FT /note= "Transmembrane region 4"

FT Region 365..383
 FT /note= "Transmembrane region 5"
 FT Region 409..428
 FT /note= "Transmembrane region 6"
 FT Region 445..463
 FT /note= "Transmembrane region 7"
 XX US2003153041-A1.
 PN 14-AUG-2003.
 PD 09-OCT-2002; 2002US-00267730.
 XX 05-APR-1991; 91US-00681702.
 PR 06-APR-1992; 92US-00864475.
 PR 06-JUN-1995; 95US-00471494.
 PR 24-NOV-1998; 98US-00199874.
 XX (GEO) GEN HOSPITAL CORP.
 PA Segre GV, Kronenberg HM, Abou-Samra A, Juppner H, Potts JT;
 XX Schipani E;
 PI WPI; 2004-051107/05.
 XX DR N-PSDB; ADH61258.
 DR XX
 XX New isolated DNA encoding parathyroid hormone receptor polypeptides,
 PT useful for diagnosing and treating disorders associated with parathyroid
 PT hormone receptors, e.g. hypercalcaemia, osteoporosis or multiple myeloma.
 XX Disclosure; SEQ ID NO 20; 71pp; English.
 XX The invention relates to parathyroid hormone (PTH) receptor and its
 CC corresponding nucleic acid sequence. The parathyroid hormone receptor
 CC polypeptides, polynucleotides and antibodies are useful for diagnosing,
 CC prognosticating and treating disorders associated with parathyroid
 CC hormone receptors, e.g. hypercalcaemia, hyperparathyroidism,
 CC osteoporosis, carcinomas of the breast, lung and prostate, epidermoid
 CC cancers of the head and neck of the oesophagus, multiple myeloma, or
 CC hypocalcaemia. The DNAs and polypeptides are also useful for screening
 CC candidate compounds for antagonistic or agonistic effects on parathyroid
 CC hormone receptor activity. The compounds are also useful in manufacturing
 CC diagnostic agents used as diagnostic tools to diagnose hypercalcaemia and
 CC to distinguish between hypercalcaemic conditions. The present sequence is
 CC rat bone PTH/PTHrP (PTH-related protein) receptor protein.
 XX SQ Sequence 591 AA;
 Query Match 94.3%; Score 410; DB 8; Length 591;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EVFDRLGMIYTVGYSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVKD 85
 DB 182 EVFDRLGMIYTVGYSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVKD 241

QY 86 AVLYSGFTLDEAERLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYWILV 145
 DB 242 AVLYSGFTLDEAERLTFEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYWILV 301

QY 146 EGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVWVGVATLANTGCDLSSGHKKW 205
 DB 302 EGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVWVGVATLANTGCDLSSGHKKW 361

QY 206 IIOVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVHY 265
 DB 362 IIOVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVHY 421

QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAIYFCNGEVSQAEIRKSNRWTLAL 325
 DB 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAIYFCNGEVSQAEIRKSNRWTLAL 481

QY 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSRPLPATTTNGHSQLPCHAKPGA 385

|||||
482 DFKKARSGSSSYGPMVSHTSVTNNGPRAGLSPLSPRLPATTNGHSQLPGHAKPGA 541
386 PATETPLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOQGWETVM 435
542 PATETPLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOQGWETVM 591
RESULT 6
ADE83416
ID ADE83416 standard; protein; 591 AA.
XX ADE83416;
AC ADE83416;
XX 29-JAN-2004 (first entry)
DT Rat Protein P25961, SEQ ID NO 11011.
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX W02003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX (GEO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; P25961.
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a rat protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 591 AA;
Query Match 92.9%; Score 404; DB 7; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 EVFDRGLMIYTVGYSMASLSTVAVLILAYFRRLHCTRNYYHMHMFLSPMLRAASIFVKD 85
DB 182 EVFDRGLMIYTVGYSMASLSTVAVLILAYFRRLHCTRNYYHMHMFLSPMLRAASIFVKD 241
QY 86 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFPLYFLATNYYWILV 145
DB 242 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFPLYFLATNYYWILV 301
QY 146 EGLYLSLIPMAFFSEKKYLMGFTIFGWLPAVFAVAVVGVVTRATLANTGWDLSGGHKKW 205
DB 302 EGLYLSLIPMAFFSEKKYLMGFTIFGWLPAVFAVAVVGVVTRATLANTGWDLSGGHKKW 361
QY 206 IIQVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 265
DB 362 IIQVPILASVVLNFIILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 421
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAVIYCFNGEVOAEIRKSWSRWTLAL 325
DB 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVAVIYCFNGEVOAEIRKSWSRWTLAL 481
QY 326 DFKRKARSGSSSYSGPMVSHTSVTNNGPRAGLSPLSPRLPATTNGHSQLPGHAKPGA 385
DB 482 DFKRKARSGSSSYSGPMVSHTSVTNNGPRAGLSPLSPRLPATTNGHSQLPGHAKPGA 541
QY 386 PATETPLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOQ 429
DB 542 PATETPLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOQ 585
RESULT 7
AA96985
ID AA96985 standard; protein; 324 AA.
XX AA96985;
XX 19-DEC-2000 (first entry)
DT Tethered PTH-1 receptor, r-del-Nt/Ct.
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
XX PTH-1 receptor; resorption; remodeling; r-delta-Nt/Ct; tethered receptor;
XX osteoporosis.
XX Rattus sp.
XX Synthetic.
XX Chimeric.
XX W0200039278-A2.
XX 06-JUL-2000.
XX 30-DEC-1999; 99WO-US031108.
XX 31-DEC-1998; 98US-0114577P.
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
XX N-PSDB; AAA51734.
XX New compound comprising an amino terminal signaling functional domain

PT linked to a carboxy-terminal binding portion of parathyroid hormone for
 PT treating mammalian conditions characterized by decreases in bone mass.
 XX
 XX Claim 22; Fig 10; 119pp; English.
 XX
 CC Compounds of the structure or formula S-(L)_n-B, R₁-S-(L)_n-R or S-(L)_n-
 CC -R, are new. S is an amino terminal signaling functional domain of
 CC parathyroid hormone (PTH); L is a linker molecule present n times (where
 CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
 CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R₁ is the
 CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
 CC sequence. The new compounds are used for treating mammalian conditions
 CC characterized by decreases in bone mass, determining rates of bone
 CC reformation, bone resorption and/or bone remodeling, treating diseases
 CC and disorders associated with decreased bone activity, increasing CAMP
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
 CC non-peptide PTH (claimed). The new compound can be administered by
 CC inhalation unlike the large native PTH or PTH-rP which avoids the need for
 CC regular injections to treat osteoporosis
 XX
 XX Sequence 324 AA;

Query Match 74.5%; Score 324; DB 3; Length 324;
 Best Local Similarity 100.0%; Pred. No. 3.6e-298;
 Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGAARIAPSLALLCCPVLSAVALVFDRLGMIYTVGYSMASLTVAVLILAYFRLH 60
 Db 1 MGAARIAPSLALLCCPVLSAVALVFDRLGMIYTVGYSMASLTVAVLILAYFRLH 60
 Qy 61 CTRNYIHHMFLSMLRAASIFVKDAVLYSGFTLDEAERLTEREELHIIAQQVPPPPAAA 120
 Db 61 CTRNYIHHMFLSMLRAASIFVKDAVLYSGFTLDEAERLTEREELHIIAQQVPPPPAAA 120
 Qy 121 GYACRVAVTFYFLATNYIIVLVEGLYLSLIFMAFFSEKKYLMGFTIFGWLPAVFV 180
 Db 121 GYACRVAVTFYFLATNYIIVLVEGLYLSLIFMAFFSEKKYLMGFTIFGWLPAVFV 180
 Qy 181 AVWVGVRATLANTCGDLSSGKKWIIQVPLASVNLNFIINIRVLATKLRNAGR 240
 Db 181 AVWVGVRATLANTCGDLSSGKKWIIQVPLASVNLNFIINIRVLATKLRNAGR 240
 Qy 241 CDRQQRKLLRSLVLPVLFVGHVYTFMALPYTEVSGTLWQIQMHYEMLFNSFGQFVA 300
 Db 241 CDRQQRKLLRSLVLPVLFVGHVYTFMALPYTEVSGTLWQIQMHYEMLFNSFGQFVA 300
 Qy 301 ILYCFNGEVAQIRKSWRWTLA 324
 Db 301 ILYCFNGEVAQIRKSWRWTLA 324

RESULT 8

AD029629

ID AD029629 standard; protein; 591 AA.

AC AD029629;

XX

XX 29-JUL-2004 (first entry)

XX Mouse GPCR PTHR1, SEQ ID NO:731.

XX

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;

XX transgenic mouse; neurological disorder; adrenal gland disorder;

XX colon disorder; intestinal disorder; cardiovascular disorder;

XX muscular disorder; blood disorder; immune disorder; bone disorder;

XX joint disorder; metabolic disorder; nutritive disorder; cancer;

XX kidney disorder; liver disorder; lung disorder; breast disorder;

XX ovary disorder; uterus disorder; prostate disorder; testis disorder;

XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;

XX thymus disorder; thyroid disorder; antiparkinsonian; antianemic;

XX cytosolic; antinflammatory; vasotropic; antidiarrhoeic; antidiabetic;

XX CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;

XX virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;

XX

dermatological; antiulcer; antithyroid; antiallergic; anorectic;
 immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
 murine; receptor.

Mus musculus.

WC2004040000-A2.

13-MAY-2004.

09-SEP-2003; 2003WO-US028226.

09-SEP-2002; 2002US-0409303P.

09-APR-2003; 2003US-0461329P.

(PRIM-) PRIMAL INC.

Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

WPI; 2004-390329/36.

N-PSDB; ADO30323.

Novel mammalian G protein coupled receptors, useful for identifying
 compounds that modulates diagnosing and treating disease condition
 associated with GPCR dysfunction e.g. autoimmune diseases, angina
 pectoris, Parkinson's disease.

Claim 151; SEQ ID NO 731; 542pp; English.

The invention relates to human and mouse G protein-coupled receptors
 (GPCRs) and nucleic acids encoding them. The invention also relates to
 sequences at least 90% identical to the GPCR proteins and nucleic acids
 of the invention; methods of treating, preventing or diagnosing diseases
 associated with GPCRs of the invention; methods of screening for
 compounds useful in the treatment of GPCR-related diseases; a transgenic
 mouse comprising a GPCR gene of the invention; a mouse comprising a
 mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 from the transgenic mice; kits comprising several mice, each of which has
 a mutation in a different GPCR gene of the invention; and kits comprising
 probes which hybridize to GPCR polynucleotides of the invention. The
 invention further discloses variants of the GPCR polypeptides and vectors
 comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 be used in the diagnosis, treatment or prevention of a wide variety of
 diseases including neurological disorders (e.g., Alzheimer's disease,
 depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 disorders of the adrenal gland; disorders of the colon or intestine
 (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 myocardial infarction); muscular disorders; blood disorders (e.g.,
 anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 diseases); and disorders of the kidney, liver, lung, breast, ovary,
 uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 thyroid (e.g., cancers). The present sequence represents a GPCR of the
 invention. Note: The full sequence data for this patent did not form part
 of the printed specification; those sequences not shown were obtained in
 electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences.

Sequence 591 AA;

Query Match 73.1%; Score 318; DB 8; Length 591;

Best Local Similarity 100.0%; Pred. No. 3e-292;

Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 EVFDRGLMIYTVGYSMASLTVAVLILAYFRLHCTRNYIHHMFLSMLRAASIFVKD 85

Db 182 EVFDRGLMIYTVGYSMASLTVAVLILAYFRLHCTRNYIHHMFLSMLRAASIFVKD 241

Qy 86 AVLYSGFTLDEAERLTEREELHIIAQQVPPPPAAAAGVACRVAVTFYFLATNYIIVL 145


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PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
XX WPI; 2000-452384/39.
XX N-PSDB; AAA51733.
XX
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass.
XX
XX Claim 22; Fig 9; 119pp; English.
XX
XX Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n
XX -R, are new. S is an amino terminal signaling functional domain of
XX parathyroid hormone (PTH); L is a linker molecule present n times (where
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
XX portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the
XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
XX sequence. The new compounds are used for treating mammalian conditions
XX characterized by decreases in bone mass, determining rates of bone
XX reformation, bone resorption and/or bone remodeling, treating diseases
XX and disorders associated with decreased tether1 activity, increasing cAMP
XX in a mammalian cell having PTH-1 receptors, or screening for a peptide or
XX non-peptide PTH (claimed). The new compound can be administered by
XX inhalation unlike the large native PTH or PTHrP which avoids the need for
XX regular injections to treat osteoporosis
XX
XX Sequence 335 AA;
XX
XX Query Match 68.7%; Score 299; DB 3; Length 335;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-274;
XX Matches 299; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 26 EVFDRLGMIYTVGYSMASLSTVAVLILAYFRRLHCTRNVIHMHMFSLFMLRAASIFVKD 85
DB 37 EVFDRLGMIYTVGYSMASLSTVAVLILAYFRRLHCTRNVIHMHMFSLFMLRAASIFVKD 96
QY 86 AVLYSGFTLDEAERLITEELHIIAQVPPPPAAAVGAGCRVAVTFPLYFLATNYYWILV 145
DB 97 AVLYSGFTLDEAERLITEELHIIAQVPPPPAAAVGAGCRVAVTFPLYFLATNYYWILV 156
QY 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVPAVAVWVGRATLANTGCWDLSSGHKKW 205
DB 157 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVPAVAVWVGRATLANTGCWDLSSGHKKW 216
QY 206 IIQVPILASVVLNFIPIRVLATKLRETNAGRCDTROQYRKLRLSTLVLVPLFGVHY 265
DB 217 IIQVPILASVVLNFIPIRVLATKLRETNAGRCDTROQYRKLRLSTLVLVPLFGVHY 276
QY 266 TVFMALPYTEVSGTLWQIQHMYELMFLNSFGQFFVAILIYFCNGEVAERKSWSRWTLA 324
DB 277 TVFMALPYTEVSGTLWQIQHMYELMFLNSFGQFFVAILIYFCNGEVAERKSWSRWTLA 335
RESULT 11
AA96987
ID ID AA96987 standard; protein; 435 AA.
XX
XX AC AA96987;
XX
XX 31-OCT-2000 (first entry)
XX
XX Human tethered PTH-1 receptor, hdelNT.
XX
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
XX PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
XX
XX Homo sapiens.
XX Synthetic.
XX Chimeric.
```

```
XX
XX WO200039278-A2.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US031108.
XX
XX 31-DEC-1998; 98US-0114577P.
XX
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
XX WPI; 2000-452384/39.
XX N-PSDB; AAA51736.
XX
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass.
XX
XX Example 4; Fig 18; 119pp; English.
XX
XX Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n
XX -R, are new. S is an amino terminal signaling functional domain of
XX parathyroid hormone (PTH); L is a linker molecule present n times (where
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
XX portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R 1 is the
XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
XX sequence. The new compounds are used for treating mammalian conditions
XX characterized by decreases in bone mass, determining rates of bone
XX reformation, bone resorption and/or bone remodeling, treating diseases
XX and disorders associated with decreased tether1 activity, increasing cAMP
XX in a mammalian cell having PTH-1 receptors, or screening for a peptide or
XX non-peptide PTH (claimed). The new compound can be administered by
XX inhalation unlike the large native PTH or PTHrP which avoids the need for
XX regular injections to treat osteoporosis
XX
XX Sequence 435 AA;
XX
XX Query Match 11.3%; Score 49; DB 3; Length 435;
XX Best Local Similarity 100.0%; Pred. No. 2.4e-37;
XX Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 121 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFT 169
DB 119 GYAGCRVAVTFFLYFLATNYYWILVEGLYLHSLIFMAFFSEKKYLWGFT 167
RESULT 12
AA96986
ID ID AA96986 standard; protein; 448 AA.
XX
XX AC AA96986;
XX
XX 31-OCT-2000 (first entry)
XX
XX Human tethered PTH-1 receptor, Tether1.
XX
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
XX PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX Peptide 1..23
XX /label= Signal_sequence
XX /note= "Human PTH-1 receptor residues 1-23"
XX Peptide 24..32
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FT Peptide /label= PTH(1-9)
 FT 33..36
 FT /label= Linker
 FT 37..448
 FT /label= PTH-1 receptor
 FT /note= "Human PTH-1 receptor residues 182-593"
 FT XX
 FT XX
 FN WO200039278-A2.

XX 06-JUL-2000.

XX 30-DEC-1999; 99WO-US031108.

XX 31-DEC-1998; 98US-0114577P.

XX (GARD/) GARDELLA T J.

XX (KRON/) KRONENBERG H M.

XX (POTT/) POTTS J T.

XX (JUEP/) JUEPPNER H.

XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX WPI; 2000-452384/39.

XX N-PSDB; AAAS1735.

XX New compound comprising an amino terminal signaling functional domain
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for
 PT treating mammalian conditions characterized by decreases in bone mass.

XX Example 4; Fig 17; 119pp; English.

XX Compounds of the structure or formula S-(L)-n-B, R₁-S-(L)-n-R or S-(L)-n
 CC -R, are new. S is an amino terminal signaling functional domain of
 CC parathyroid hormone (PTH); L is a linker molecule present n times (where
 CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
 CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R₁ is the
 CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
 CC sequence. The new compounds are used for treating mammalian conditions
 CC characterized by decreases in bone mass, determining rates of bone
 CC reformation, bone resorption and/or bone remodeling, treating diseases
 CC and disorders associated with decreased tether activity, increasing CAMP
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
 CC non-peptide PTH (claimed). The new compound can be administered by
 CC inhalation unlike the large native PTH or PTHrp which avoids the need for
 CC regular injections to treat osteoporosis

XX Sequence 448 AA;

Query Match 11.3%; Score 49; DB 3; Length 448;

Best Local Similarity 100.0%; Pred. No. 2.5e-37;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GYAGCRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169

DB 132 GYAGCRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 180

RESULT 13

AAAY96988

ID AAY96988 standard; protein; 450 AA.

XX AAAY96988;

XX 31-OCT-2000 (first entry)

XX Human tethered PTH-1 receptor, Tether-R11.

XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
 XX PTH-1 receptor; resorption; remodeling; tether-R11; osteoporosis; ss.

XX Homo sapiens.

XX Synthetic.

XX Chimeric.

XX Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Signal sequence
 FT /note= "Human PTH-1 receptor residues 1-23"
 FT 24..34
 FT /label= PTH(1-11)
 FT 35..38
 FT /label= Linker
 FT 39..450
 FT /label= PTH-1 receptor
 FT /note= "Human PTH-1 receptor residues 182-593"
 XX WO200039278-A2.

XX 06-JUL-2000.

XX 30-DEC-1999; 99WO-US031108.

XX 31-DEC-1998; 98US-0114577P.

XX (GARD/) GARDELLA T J.

XX (KRON/) KRONENBERG H M.

XX (POTT/) POTTS J T.

XX (JUEP/) JUEPPNER H.

XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX WPI; 2000-452384/39.

XX N-PSDB; AAAS1737.

XX New compound comprising an amino terminal signaling functional domain
 PT linked to a carboxy-terminal binding portion of parathyroid hormone for
 PT treating mammalian conditions characterized by decreases in bone mass.

XX Example 4; Fig 19; 119pp; English.

XX Compounds of the structure or formula S-(L)-n-B, R₁-S-(L)-n-R or S-(L)-n
 CC -R, are new. S is an amino terminal signaling functional domain of
 CC parathyroid hormone (PTH); L is a linker molecule present n times (where
 CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
 CC portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R₁ is the
 CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
 CC sequence. The new compounds are used for treating mammalian conditions
 CC characterized by decreases in bone mass, determining rates of bone
 CC reformation, bone resorption and/or bone remodeling, treating diseases
 CC and disorders associated with decreased tether activity, increasing CAMP
 CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
 CC non-peptide PTH (claimed). The new compound can be administered by
 CC inhalation unlike the large native PTH or PTHrp which avoids the need for
 CC regular injections to treat osteoporosis

XX Sequence 450 AA;

Query Match 11.3%; Score 49; DB 3; Length 450;

Best Local Similarity 100.0%; Pred. No. 2.5e-37;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GYAGCRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169

DB 134 GYAGCRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 182

RESULT 14

AAAW73317

ID AAW73317 standard; protein; 593 AA.

XX AAW73317;

XX 08-FEB-1999 (first entry)

XX Human Parathyroid hormone receptor.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2005, 06:19:15 ; Search time 28 Seconds
(without alignments)
1159.727 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 435

Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGARPPPLQEGWETVM 435

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgm2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgm2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/6A COMB.pep.*
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5: /cgm2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	410	94.3	591	2	US-08-468-249A-20
2	49	11.3	593	2	US-08-468-249A-21
3	49	11.3	593	4	US-09-631-603-21
4	49	11.3	593	4	US-09-826-509-563
5	48	11.0	207	4	US-08-811-519-31
6	34	7.8	515	2	US-08-468-249A-18
7	34	7.8	585	1	US-08-142-439A-6
8	34	7.8	585	2	US-08-142-551B-125
9	34	7.8	585	2	US-08-869-477-6
10	34	7.8	585	2	US-08-468-249A-19
11	31	7.1	593	3	US-08-468-011A-24
12	31	7.1	593	3	US-08-236-468A-24
13	29	6.7	52	3	US-08-468-011A-14
14	29	6.7	52	3	US-09-236-468A-14
15	28	6.4	536	4	US-09-449-632-2
16	25	5.7	60	3	US-08-468-011A-10
17	25	5.7	60	3	US-09-236-468A-10
18	25	5.7	575	4	US-03-449-632-5
19	24	5.5	25	1	US-07-864-475A-13
20	24	5.5	25	2	US-08-468-249A-13
21	24	5.5	26	1	US-07-864-475A-8
22	24	5.5	26	2	US-08-468-249A-8
23	19	4.4	19	1	US-07-864-475A-7
24	19	4.4	19	2	US-08-468-249A-7
25	18	4.1	19	1	US-07-864-475A-6
26	18	4.1	19	2	US-08-468-249A-6
27	18	4.1	60	3	US-08-468-011A-9

28 18 4.1 60 3 US-09-236-468A-9 Sequence 9, Appli
29 18 4.1 541 3 US-08-468-011A-2 Sequence 2, Appli
30 18 4.1 541 3 US-09-236-468A-2 Sequence 2, Appli
31 18 4.1 541 5 PCT-US95-07085-2 Sequence 2, Appli
32 18 4.1 542 4 US-09-449-632-4 Sequence 4, Appli
33 18 4.1 550 4 US-09-631-603-20 Sequence 20, Appli
34 18 4.1 550 4 US-09-826-509-565 Sequence 565, App
35 15 3.4 60 3 US-08-468-011A-19 Sequence 19, Appli
36 15 3.4 60 3 US-08-468-011A-20 Sequence 20, Appli
37 15 3.4 60 3 US-09-236-468A-19 Sequence 19, Appli
38 15 3.4 60 3 US-09-236-468A-20 Sequence 20, Appli
39 14 3.2 60 3 US-08-468-011A-12 Sequence 12, Appli
40 14 3.2 207 4 US-09-236-468A-12 Sequence 12, Appli
41 14 3.2 207 4 US-08-811-519-30 Sequence 30, Appli
42 14 3.2 440 4 US-09-631-603-22 Sequence 22, Appli
43 14 3.2 440 4 US-09-826-509-567 Sequence 567, App
44 14 3.2 449 1 US-08-142-439A-5 Sequence 5, Appli
45 14 3.2 449 2 US-08-869-477-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-468-249A-20
; Sequence 20, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-249A-20

Query Match 94.3%; Score 410; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 EVFRLGMIYTVGYSMISLSTVAVLILAYFRRLLHCTRNYYHMHFSLFEMLRASIFVKD 85
Db 182 EVFRLGMIYTVGYSMISLSTVAVLILAYFRRLLHCTRNYYHMHFSLFEMLRASIFVKD 241
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Db 242 AVLYSGFTLDAERLTDEEELHIIAQVPPPPAAAAVGYAGCRVAVTFFLYFLATNYYWILV 301
Qy 146 EGLYLHSLIFMAFFSEKKYLMGFTIFGKGLPAVFVAVVWGVRAFLANTGWDLSGGHKW 205
Db 302 EGLYLHSLIFMAFFSEKKYLMGFTIFGKGLPAVFVAVVWGVRAFLANTGWDLSGGHKW 361
Qy 206 IIQVPIILASVVLNFIILFNIIRVLATKLRNAGRCRDTQOYRKLRLSTLVLVPLFGVHY 265
Db 362 IIQVPIILASVVLNFIILFNIIRVLATKLRNAGRCRDTQOYRKLRLSTLVLVPLFGVHY 421
Qy 266 TVFMALPTEVSGTLWQIQMHEMLFNSFOGFFVAILIYFCNGEVAEIRKSNRWTAL 325
Db 422 TVFMALPTEVSGTLWQIQMHEMLFNSFOGFFVAILIYFCNGEVAEIRKSNRWTAL 481
Qy 326 DFKKKARSGSSSYGYGPMVSHSTVTVNGPRAGLSPLSPRLPPATTNGHSQLPGHAKPGA 385
Db 482 DFKKKARSGSSSYGYGPMVSHSTVTVNGPRAGLSPLSPRLPPATTNGHSQLPGHAKPGA 541
Qy 386 PATETETLPVTMAYPKDDGFLNGSCGLDEASGARPPPLQLQGWTVM 435
Db 542 PATETETLPVTMAYPKDDGFLNGSCGLDEASGARPPPLQLQGWTVM 591

RESULT 2
US-08-468-249A-21
; Sequence 21, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-468-249A-21
Query Match 11.3%; Score 49; DB 2; Length 593;
Best Local Similarity 100.0%; Pred. No. 4.4e-36;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 121 GYAGCRVAVTFFLYFLATNYYWILVGLYLHSLIFMAFFSEKKYLMGFT 169
Db 277 GYAGCRVAVTFFLYFLATNYYWILVGLYLHSLIFMAFFSEKKYLMGFT 325

RESULT 3
US-09-631-603-21
; Sequence 21, Application US/09631603
; Patent No. 6733990
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Lloyd, Clare
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: 15571, A No. 6733990el GPCR-like Molecule of the
; TITLE OF INVENTION: Secretin-Like Family and Uses Thereof
; FILE REFERENCE: 5800-48A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US/09/631,603
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/146,916
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-631-603-21

Query Match 11.3%; Score 49; DB 4; Length 593;
Best Local Similarity 100.0%; Pred. No. 4.4e-36;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 121 GYAGCRVAVTFFLYFLATNYYWILVGLYLHSLIFMAFFSEKKYLMGFT 169
Db 277 GYAGCRVAVTFFLYFLATNYYWILVGLYLHSLIFMAFFSEKKYLMGFT 325

RESULT 4
US-09-826-509-563
; Sequence 563, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patentin Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-563

Query Match 11.3%; Score 49; DB 4; Length 593;
Best Local Similarity 100.0%; Pred. No. 4.4e-36;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFPLFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169
Db 277 GYACRVAVTFPLFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 325

RESULT 5

US-08-811-519-31
; Sequence 31, Application US/08811519B
; Patent No. 6630345
; GENERAL INFORMATION:
; APPLICANT: Petrenko, Alexandre
; TITLE OF INVENTION: CALCIUM INDEPENDENT RECEPTOR OF ALPHA-LATROTOXIN,
; FILE REFERENCE: 1049-1-007
; CURRENT APPLICATION NUMBER: US/08/811,519B
; CURRENT FILING DATE: 1997-03-04
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-811-519-31

Query Match 11.0%; Score 48; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.4e-35;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 YACRVAVTFPLFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169
Db 55 YACRVAVTFPLFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 102

RESULT 6

US-08-468-249A-18
; Sequence 18, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frazer, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 515 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-249A-18

Query Match 7.8%; Score 34; DB 2; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 NFILFINIIRVLATKLRETNAGRCDDTRQQYRKLL 251
Db 368 NFILFINIIRVLATKLRETNAGRCDDTRQQYRKLL 401

RESULT 7

US-08-142-439A-6
; Sequence 6, Application US/08142439A
; Patent No. 5670360
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5670360o No. 5670360disk of No. 5670360th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439A
; FILING DATE: 24-NOV-93
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Didelphis virginiana
US-08-142-439A-6

Query Match 7.8%; Score 34; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 NFILFINIIRVLATKLRETNAGRCDDTRQQYRKLL 251

Db 368 NFILFINIRVLATKLRETNAGCDTRQYRKLL 401

RESULT 8

US-08-142-551B-125
Sequence 125, Application US/08142551B
Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,551B
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-7400
TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..585
OTHER INFORMATION: /note= "PTH receptor"

US-08-142-551B-125

Query Match 7.8%; Score 34; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 NFILFINIRVLATKLRETNAGCDTRQYRKLL 251
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Db 368 NFILFINIRVLATKLRETNAGCDTRQYRKLL 401

RESULT 9

US-08-869-477-6
Sequence 6, Application US/08869477
Patent No. 5846747
GENERAL INFORMATION:
APPLICANT: Thorens, Bernard
TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1

; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5846747to No. 5846747disk of No. 5846747th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-8201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,477
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439
; FILING DATE: 24-NOV-93
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Didelphis virginiana
; US-08-869-477-6

Query Match 7.8%; Score 34; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 NFILFINIRVLATKLRETNAGCDTRQYRKLL 251
|||||

Db 368 NFILFINIRVLATKLRETNAGCDTRQYRKLL 401

RESULT 10

US-08-468-249A-19
Sequence 19, Application US/08468249A
Patent No. 5886148
GENERAL INFORMATION:
APPLICANT: Segre et al., Gino V.
TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-249A-19

Query Match 7.8%; Score 34; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 NFILFINIIRVLATKLRNTAGRCDTROQVRKLL 251
DB 368 NFILFINIIRVLATKLRNTAGRCDTROQVRKLL 401

RESULT 11
US-08-468-011A-24
; Sequence 24, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
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; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-24

Query Match 7.1%; Score 31; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 QMHEMLFNSFGQFFVAILIYFCNCGEVQAEI 314
DB 8 QMHEMLFNSFGQFFVAILIYFCNCGEVQAEI 38

RESULT 12
US-09-236-468A-24
; Sequence 24, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236,468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Didelphis virginiana
; US-09-236-468A-24

Query Match 7.1%; Score 31; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 QMHEMLFNSFGQFFVAILIYFCNCGEVQAEI 314
DB 8 QMHEMLFNSFGQFFVAILIYFCNCGEVQAEI 38

RESULT 13
US-08-468-011A-14
; Sequence 14, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
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; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-14

Query Match 6.7%; Score 29; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 8.3e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 INIIRVLATKLRITNAGRCDTROQYRKLL 251
Db 1 INIIRVLATKLRITNAGRCDTROQYRKLL 29

RESULT 14
US-09-236-468A-14
; Sequence 14, Application US/09236468A
; Patent No. 6338951
; GENERAL INFORMATION:
; APPLICANT: Soppet et al.
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTG74
; FILE REFERENCE: PF201D1
; CURRENT APPLICATION NUMBER: US/09/236.468A
; CURRENT FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/468,011
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Didelphis virginiana
US-09-236-468A-14

Query Match 6.7%; Score 29; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 8.3e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 223 INIIRVLATKLRITNAGRCDTROQYRKLL 251
Db 1 INIIRVLATKLRITNAGRCDTROQYRKLL 29

RESULT 15
US-09-449-632-2
; Sequence 2, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHrR and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
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; ORGANISM: zebrafish
US-09-449-632-2
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Query Match 6.4%; Score 28; DB 4; Length 536;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 224 NIIRVLATKLRITNAGRCDTROQYRKLL 251
Db 334 NIIRVLATKLRITNAGRCDTROQYRKLL 361
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

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Title: US-09-869-565-2

Perfect score: 435

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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	404	92.9	591	9	US-09-943-446-7
3	318	73.1	591	9	US-09-943-446-8
4	49	11.3	593	9	US-09-943-446-9
5	49	11.3	593	10	US-09-826-509-563
6	49	11.3	593	14	US-10-225-567A-229
7	49	11.3	593	14	US-10-267-730-21
8	49	11.3	593	16	US-10-723-860-1006
9	49	11.3	593	17	US-10-925-095-563
10	49	11.3	593	17	US-10-505-486-13
11	49	11.3	595	9	US-09-943-446-6
					Sequence 20, Appl
					Sequence 7, Appli
					Sequence 8, Appli
					Sequence 9, Appli
					Sequence 563, App
					Sequence 229, App
					Sequence 21, Appl
					Sequence 1006, Ap
					Sequence 563, App
					Sequence 13, Appl
					Sequence 6, Appli

12	43	9.9	964	14	US-10-017-161-710	Sequence 710, App
13	43	9.9	964	15	US-10-292-798-622	Sequence 622, App
14	34	7.8	515	14	US-10-267-730-18	Sequence 18, Appl
15	34	7.8	585	14	US-10-267-730-19	Sequence 19, Appl
16	31	7.1	59	9	US-09-996-569-24	Sequence 24, Appl
17	31	7.1	59	17	US-10-921-218-24	Sequence 24, Appl
18	29	6.7	52	9	US-09-996-569-14	Sequence 14, Appl
19	29	6.7	52	17	US-10-921-218-14	Sequence 14, Appl
20	28	6.7	536	14	US-10-372-095-2	Sequence 2, Appli
21	25	5.7	60	9	US-09-996-569-10	Sequence 10, Appl
22	25	5.7	60	17	US-10-921-218-10	Sequence 10, Appl
23	25	5.7	575	14	US-10-372-095-5	Sequence 5, Appli
24	24	5.5	25	14	US-10-267-730-13	Sequence 13, Appl
25	24	5.5	26	14	US-10-267-730-8	Sequence 8, Appli
26	19	4.4	19	14	US-10-225-567A-1231	Sequence 1231, Ap
27	19	4.4	19	14	US-10-267-730-7	Sequence 7, Appli
28	19	4.4	19	14	US-10-267-730-22	Sequence 22, Appl
29	18	4.1	19	14	US-10-267-730-6	Sequence 6, Appli
30	18	4.1	60	9	US-09-996-569-9	Sequence 9, Appli
31	18	4.1	60	17	US-10-921-218-9	Sequence 9, Appli
32	18	4.1	541	9	US-09-996-569-2	Sequence 2, Appli
33	18	4.1	541	17	US-10-921-218-2	Sequence 4, Appli
34	18	4.1	542	14	US-10-372-095-4	Sequence 109, App
35	18	4.1	546	14	US-10-014-162-109	Sequence 565, App
36	18	4.1	550	10	US-09-826-505-565	Sequence 227, App
37	18	4.1	550	14	US-10-225-567A-227	Sequence 526, App
38	18	4.1	550	15	US-10-295-027-526	Sequence 851, App
39	18	4.1	550	15	US-10-295-027-851	Sequence 2139, Ap
40	18	4.1	550	16	US-10-723-860-2139	Sequence 565, App
41	18	4.1	550	17	US-10-925-095-565	Sequence 524, App
42	18	4.1	561	15	US-10-295-027-524	Sequence 23, Appl
43	15	3.4	18	14	US-10-267-730-23	Sequence 19, Appl
44	15	3.4	60	9	US-09-996-569-19	Sequence 20, Appl
45	15	3.4	60	9	US-09-996-569-20	

ALIGNMENTS

RESULT 1

US-10-267-730-20
; Sequence 20, Application US/10267730
; Publication No. US200301053041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-267-730-20

Query Match	94.3%	Score	410;	DB	14;	Length	591;
Best Local Similarity	100.0%	Pred. No.	0;				
Matches	410;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;
Qy	26	EVFDRGLMITYTGVGYSMSLASLTAVLILAYFRLHCTRYNIHMHMFLSPMLRAASIFVKD	85				
Db	182	EVFDRGLMITYTGVGYSMSLASLTAVLILAYFRLHCTRYNIHMHMFLSPMLRAASIFVKD	241				
Qy	86	AVLYSGFTLDEARLTTEELHIIAQVPPPPAAAAGVACGRVATFFFLYFLATNYWILV	145				

Db 242 AVLYSGFTLDEAERLTSEELHIIAQVPPPPAAAVGAGCRVAVTFFLYFLATNYWILV 301
Qy 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVVATLANTGCWDLSGGHKW 205
Db 302 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVVATLANTGCWDLSGGHKW 361
Qy 206 IIQVPIILASVVLNFIILFINIRVLATKLRNAGRCDDTROQYRKLRLSTLVLPLFGVHY 265
Db 362 IIQVPIILASVVLNFIILFINIRVLATKLRNAGRCDDTROQYRKLRLSTLVLPLFGVHY 421
Qy 266 TVFMALPYTEVSGTLMQIQMHYEMLFNSFGQFFVAIYFCNCEVQAEIRKSWRWTAL 325
Db 422 TVFMALPYTEVSGTLMQIQMHYEMLFNSFGQFFVAIYFCNCEVQAEIRKSWRWTAL 481
Qy 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTTNGHSQLPGHAKPGA 385
Db 482 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTTNGHSQLPGHAKPGA 541
Qy 386 PATETETPLVTMAVPKDDGFLNGSCGLDEEASGSRPPPLLOEGWETVM 435
Db 542 PATETETPLVTMAVPKDDGFLNGSCGLDEEASGSRPPPLLOEGWETVM 591

RESULT 2

US-09-943-446-7

; Sequence 7, Application US/09943446

; Patent No. US20020146777A1

; GENERAL INFORMATION:

; APPLICANT: Pfizer Inc.

; APPLICANT: Castleberry, Tessa A.

; APPLICANT: Lu, Bihong

; APPLICANT: Owen, Thomas A.

; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor

; FILE REFERENCE: PC10891AGPR

; CURRENT APPLICATION NUMBER: US/09/943,446

; CURRENT FILING DATE: 2001-08-30

; PRIOR APPLICATION NUMBER: US 60/229,170

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 591

; TYPE: PRT

; ORGANISM: Rattus No. US20020146777Alvegicus

; US-09-943-446-7

Query Match 92.9%; Score 404; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 EVFDRGLMIYTVGYSMASLITVAVLILAYFRRLHCTRTNYIHHMFLSPMLRAASIFVKD 85
Db 182 EVFDRGLMIYTVGYSMASLITVAVLILAYFRRLHCTRTNYIHHMFLSPMLRAASIFVKD 241
Qy 86 AVLYSGFTLDEAERLTSEELHIIAQVPPPPAAAVGAGCRVAVTFFLYFLATNYWILV 145
Db 242 AVLYSGFTLDEAERLTSEELHIIAQVPPPPAAAVGAGCRVAVTFFLYFLATNYWILV 301
Qy 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVVATLANTGCWDLSGGHKW 205
Db 302 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVVATLANTGCWDLSGGHKW 361
Qy 206 IIQVPIILASVVLNFIILFINIRVLATKLRNAGRCDDTROQYRKLRLSTLVLPLFGVHY 265
Db 362 IIQVPIILASVVLNFIILFINIRVLATKLRNAGRCDDTROQYRKLRLSTLVLPLFGVHY 421
Qy 266 TVFMALPYTEVSGTLMQIQMHYEMLFNSFGQFFVAIYFCNCEVQAEIRKSWRWTAL 325
Db 422 TVFMALPYTEVSGTLMQIQMHYEMLFNSFGQFFVAIYFCNCEVQAEIRKSWRWTAL 481
Qy 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTTNGHSQLPGHAKPGA 385

Db 482 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPPATTTNGHSQLPGHAKPGA 541
Qy 386 PATETETPLVTMAVPKDDGFLNGSCGLDEEASGSRPPPLLOE 429
Db 542 PATETETPLVTMAVPKDDGFLNGSCGLDEEASGSRPPPLLOE 585

RESULT 3

US-09-943-446-8

; Sequence 8, Application US/09943446

; Patent No. US20020146777A1

; GENERAL INFORMATION:

; APPLICANT: Pfizer Inc.

; APPLICANT: Castleberry, Tessa A.

; APPLICANT: Lu, Bihong

; APPLICANT: Owen, Thomas A.

; APPLICANT: Smock, Steven L.

; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor

; FILE REFERENCE: PC10891AGPR

; CURRENT APPLICATION NUMBER: US/09/943,446

; CURRENT FILING DATE: 2001-08-30

; PRIOR APPLICATION NUMBER: US 60/229,170

; PRIOR FILING DATE: 2000-08-30

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 591

; TYPE: PRT

; ORGANISM: Mus Musculus

; US-09-943-446-8

Query Match 73.1%; Score 318; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.4e-292;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 EVFDRGLMIYTVGYSMASLITVAVLILAYFRRLHCTRTNYIHHMFLSPMLRAASIFVKD 85
Db 182 EVFDRGLMIYTVGYSMASLITVAVLILAYFRRLHCTRTNYIHHMFLSPMLRAASIFVKD 241
Qy 86 AVLYSGFTLDEAERLTSEELHIIAQVPPPPAAAVGAGCRVAVTFFLYFLATNYWILV 145
Db 242 AVLYSGFTLDEAERLTSEELHIIAQVPPPPAAAVGAGCRVAVTFFLYFLATNYWILV 301
Qy 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVVATLANTGCWDLSGGHKW 205
Db 302 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVGVVATLANTGCWDLSGGHKW 361
Qy 206 IIQVPIILASVVLNFIILFINIRVLATKLRNAGRCDDTROQYRKLRLSTLVLPLFGVHY 265
Db 362 IIQVPIILASVVLNFIILFINIRVLATKLRNAGRCDDTROQYRKLRLSTLVLPLFGVHY 421
Qy 266 TVFMALPYTEVSGTLMQIQMHYEMLFNSFGQFFVAIYFCNCEVQAEIRKSWRWTAL 325
Db 422 TVFMALPYTEVSGTLMQIQMHYEMLFNSFGQFFVAIYFCNCEVQAEIRKSWRWTAL 481
Qy 326 DFKRKARSGSSSYSGPM 343
Db 482 DFKRKARSGSSSYSGPM 499

RESULT 4

US-09-943-446-9

; Sequence 9, Application US/09943446

; Patent No. US20020146777A1

; GENERAL INFORMATION:

; APPLICANT: Pfizer Inc.

; APPLICANT: Castleberry, Tessa A.

; APPLICANT: Lu, Bihong

; APPLICANT: Owen, Thomas A.

; APPLICANT: Smock, Steven L.

; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor

; FILE REFERENCE: PC10891AGPR

```
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-943-446-9

Query Match      11.3%; Score 49; DB 9; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      121  GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 169
      |||||||
Db      277  GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 325

RESULT 5
US-09-826-509-563
; Sequence 563, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinema, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-563

Query Match      11.3%; Score 49; DB 10; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      121  GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 169
      |||||||
Db      277  GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 325

RESULT 6
US-10-225-567A-229
; Sequence 229, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burwer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 229
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; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-229

Query Match      11.3%; Score 49; DB 14; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      121  GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 169
      |||||||
Db      277  GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 325

RESULT 7
US-10-267-730-21
; Sequence 21, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-730-21

Query Match      11.3%; Score 49; DB 14; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      121  GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 169
      |||||||
Db      277  GYACRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWGFT 325

RESULT 8
US-10-723-860-1006
; Sequence 1006, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882, 0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1006
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-1006

Query Match      11.3%; Score 49; DB 16; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
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Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169
Db 277 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 325

RESULT 9

US-10-925-095-563
; Sequence 563, Application US/10925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinema, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-925-095-563

Query Match 11.3%; Score 49; DB 17; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169
Db 277 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 325

RESULT 10

US-10-505-486-13
; Sequence 13, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 13
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Human
US-10-505-486-13

Query Match 11.3%; Score 49; DB 17; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169
Db 277 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 325

RESULT 11

US-09-943-446-6
; Sequence 6, Application US/09943446
; Patent No. US2002014677A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Castleberry, Tessa A.
; APPLICANT: Lu, Bihong
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor
; FILE REFERENCE: PC10891AGPR
; CURRENT APPLICATION NUMBER: US/09/943,446
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,170
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Canis Familiaris
US-09-943-446-6

Query Match 11.3%; Score 49; DB 9; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169
Db 276 GYACRVAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 324

RESULT 12

US-10-017-161-710
; Sequence 710, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 710
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-710

Query Match 9.9%; Score 43; DB 14; Length 964;
Best Local Similarity 100.0%; Pred. No. 2.2e-31;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 VAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 169
Db 557 VAVTFFLYFLATNYWILVEGLYHLSLIFMAFFSEKKYLGFT 599

RESULT 13

US-10-292-798-622
; Sequence 622, Application US/10292798
; Publication No. US2003023583A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO

; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 622
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-622

Query Match 9.9%; Score 43; DB 15; Length 964;
Best Local Similarity 100.0%; Pred. No. 2.2e-31;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 VAVTFEFLYFLATNYWILVEGLYHSLIFMAFFSEKKYLGFT 169
Db 557 VAVTFEFLYFLATNYWILVEGLYHSLIFMAFFSEKKYLGFT 599

RESULT 14

US-10-267-730-18
; Sequence 18, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-18

Query Match 7.8%; Score 34; DB 14; Length 515;
Best Local Similarity 100.0%; Pred. No. 4.2e-23;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 251
Db 368 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 401

RESULT 15

US-10-267-730-19
; Sequence 19, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina

; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-19

Query Match 7.8%; Score 34; DB 14; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.7e-23;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 251
Db 368 NFILFINIIRVLATKLRETNAGRCDTROQYRKLL 401

Search completed: July 4, 2005, 06:36:45
Job time : 81 secs

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QY 326 DEKKKARSGSSSYSGPMVSHTSVTNVPRAGLSLPLSPRLPATTTNGHSQLPCHAKPGA 385
Db 482 DFKRKARSGSSSYSGPMVSHTSVTNVPRAGLSLPLSPRLPATTTNGHSQLPCHAKPGA 541
QY 386 PATETETLPVTMAVPKDDGFLNGSCSLDEEASGSARPPPLQOE 429
Db 542 PATETETLPVTMAVPKDDGFLNGSCSLDEEASGSARPPPLQOE 585

RESULT 2
S44203
parathyroid hormone-related peptide receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S44203
R;Karperien, M.; van Dijk, T.B.; Hoelmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boonstra
submitted to the EMBL Data Library, April 1994
A;Description: Expression pattern of parathyroid hormone/parathyroid hormone related pep
A;Reference number: S44203
A;Accession: S44203
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-591 <KAR>
A;Cross-references: UNIPROT:P41593; EMBL:X78936; NID:9474828; PIDN:CAA55536.1; PID:94748
C;Superfamily: glucagon receptor

Query Match 73.1%; Score 318; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 7.2e-309;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EVFDRLGMIYTVGYSMSLASLTAVALLAYFRLHCTRTNYIHMHMFLSFMRLRAASIFVKD 85
Db 182 EVFDRLGMIYTVGYSMSLASLTAVALLAYFRLHCTRTNYIHMHMFLSFMRLRAASIFVKD 241
QY 86 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFPLYFLATNYWILV 145
Db 242 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFPLYFLATNYWILV 301
QY 146 EGYLHLSLIFMAFFSEKKYLGWFTIFGWGLPAFVAVVWGVVRATLANTGCWDLSSSHKKW 205
Db 302 EGYLHLSLIFMAFFSEKKYLGWFTIFGWGLPAFVAVVWGVVRATLANTGCWDLSSSHKKW 361
QY 206 IIOVPILASVVLNFIINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLPFGVHY 265
Db 362 IIOVPILASVVLNFIINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLPFGVHY 421
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVVAIIYCFCN 307
Db 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVVAIIYCFCN 463

RESULT 3
S44203
parathyroid hormone-related peptide receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S44203
R;Karperien, M.; van Dijk, T.B.; Hoelmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boonstra
submitted to the EMBL Data Library, April 1994
A;Description: Expression pattern of parathyroid hormone/parathyroid hormone related pep
A;Reference number: S44203
A;Accession: S44203
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-591 <KAR>
A;Cross-references: UNIPROT:P41593; EMBL:X78936; NID:9474828; PIDN:CAA55536.1; PID:94748
C;Superfamily: glucagon receptor

Query Match 73.1%; Score 318; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 7.2e-309;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EVFDRLGMIYTVGYSMSLASLTAVALLAYFRLHCTRTNYIHMHMFLSFMRLRAASIFVKD 85
Db 182 EVFDRLGMIYTVGYSMSLASLTAVALLAYFRLHCTRTNYIHMHMFLSFMRLRAASIFVKD 241
QY 86 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFPLYFLATNYWILV 145
Db 242 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFPLYFLATNYWILV 301
QY 146 EGYLHLSLIFMAFFSEKKYLGWFTIFGWGLPAFVAVVWGVVRATLANTGCWDLSSSHKKW 205
Db 302 EGYLHLSLIFMAFFSEKKYLGWFTIFGWGLPAFVAVVWGVVRATLANTGCWDLSSSHKKW 361
QY 206 IIOVPILASVVLNFIINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLPFGVHY 265
Db 362 IIOVPILASVVLNFIINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLPFGVHY 421
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVVAIIYCFCN 307
Db 422 TVFMALPYTEVSGTLWQIQMHYEMLFNSFGQFFVVAIIYCFCN 463

RESULT 4
S44191
parathyroid hormone/PTH-related peptide receptor - human
N;Alternate names: parathyroid hormone/parathyroid hormone related peptide receptor
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: I38139; A49191; I38113; G01562; S29610
R;Schipani, E.; Weinstein, L.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuhmann, M.;
Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Jueppner, H.
J. Clin. Endocrinol. Metab. 80, 1611-1621, 1995
A;Title: Pseudohypoparathyroidism type 1b is not caused by mutations in the coding exons
A;Reference number: I38139; MUID:95263723; PMID:7745008
A;Accession: I38139
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-593 <RES>
A;Cross-references: UNIPROT:Q03431; EMBL:U22409; NID:9897594; PIDN:AA860657.1; PID:989759;
R;Schipani, E.; Karsa, H.; Karaplis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V.
Endocrinology 132, 2157-2165, 1993
A;Title: Identical complementary deoxyribonucleic acids encode a human renal and bone par
A;Reference number: A49191; MUID:93238641; PMID:8386612
A;Accession: A49191
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-593 <SCH>
A;Cross-references: GB:I04308; NID:9190721; PIDN:AAA36525.1; PID:9190722
A;Note: sequence extracted from NCBI backbone (NCBIN:I30233, NCBIP:I30234)
R;Schneider, H.; Feven, J.H.; Seuwen, K.; Movva, N.R.
Eur. J. Pharmacol. 246, 149-155, 1993
A;Title: Cloning and functional expression of a human parathyroid hormone receptor.
A;Reference number: I38113; MUID:93387403; PMID:8397094
A;Accession: I38113
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-593 <BE2>
A;Cross-references: EMBL:X68596; NID:9396812; PIDN:CAA48589.1; PID:g396813
R;Levine, M.
submitted to the EMBL Data Library, November 1994
A;Reference number: G07787
A;Accession: G01562
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-593 <LEV>
A;Cross-references: EMBL:U17418; NID:9596129; PIDN:AAA56774.1; PID:g596130
C;Genetics:
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A;Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 45/3
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: J02532
R;Jiang, S.; Ulrich, C.
Biochem. Biophys. Res. Commun. 207, 883-890, 1995
A;Title: Molecular cloning and functional expression of a human pancreatic secretin receptor
A;Reference number: J02532; MUID:95169147; PMID:7864894
A;Accession: J02532
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
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A;Cross-references: UNIPROT:P47872; EMBL:U020178; NID:g662795; PIDN:AAC50106.1; PID:g662795
A;Experimental source: pancreas
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A;Gene: GDB:SCTR
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A;Map position: 2q14.1-2q14.1
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RESULT 5
A39286
parathyroid hormone / parathyroid hormone-related peptide - North American opossum
C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossum)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004
C;Accession: A39286
R;Jueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.; K
Science 254, 1024-1026, 1991
A;Title: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-rel
A;Reference number: A39286; MUID:92054592; PMID:1658941
A;Accession: A39286
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-585 <JUE>
A;Cross-references: UNIPROT:P25107; GB:M74445
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 7.8%; Score 34; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.4e-25; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 NFILFINIIRVLATKLRETNAGRCDTQQRKLL 251
|||||
Db 368 NFILFINIIRVLATKLRETNAGRCDTQQRKLL 401
|||||

RESULT 6
A57519
parathyroid hormone receptor 2 precursor - human
N;Alternate names: PTH2 receptor
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
C;Accession: A57519
R;Udin, T.B.; Gruber, C.; Bonner, T.I.
J. Biol. Chem. 270, 15455-15458, 1995
A;Title: Identification and functional expression of a receptor selectively recognizing
A;Reference number: A57519; MUID:95318121; PMID:7797535
A;Accession: A57519
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-550 <USD>
A;Cross-references: UNIPROT:P49190; GB:U25128; NID:g887966; PIDN:AAC50157.1; PID:g887967
C;Genetics:
A;Gene: GDB:PTH2R; PTHR2R
A;Cross-references: GDB:731977; OMIM:601469
A;Map position: 2q33-2q33
C;Superfamily: glucagon receptor
C;Keywords: hormone receptor

Query Match 4.1%; Score 18; DB 2; Length 550;
Best Local Similarity 100.0%; Pred. No. 2.1e-09; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 YFLATNYWILVEGLYLH 151
|||||
Db 245 YFLATNYWILVEGLYLH 262
|||||

RESULT 7

JC2532
secretin receptor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: J02532
R;Jiang, S.; Ulrich, C.
Biochem. Biophys. Res. Commun. 207, 883-890, 1995
A;Title: Molecular cloning and functional expression of a human pancreatic secretin receptor
A;Reference number: J02532; MUID:95169147; PMID:7864894
A;Accession: J02532
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-440 <JIA>
A;Cross-references: UNIPROT:P47872; EMBL:U020178; NID:g662795; PIDN:AAC50106.1; PID:g662795
A;Experimental source: pancreas
C;Genetics:
A;Gene: GDB:SCTR
A;Cross-references: GDB:270546; OMIM:182098
A;Map position: 2q14.1-2q14.1
C;Superfamily: glucagon receptor

Query Match 3.2%; Score 14; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.7e-05; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 FRELHCTRYNIHMH 69
|||||
Db 167 FRELHCTRYNIHMH 180
|||||

RESULT 8
S16319
secretin receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S16319
R;Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Negata, S.
EMBO J. 10, 1635-1641, 1991
A;Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.
A;Reference number: S16319; MUID:91266890; PMID:1646711
A;Accession: S16319
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-449 <ISH>
A;Cross-references: UNIPROT:P23811; EMBL:X59132; NID:g57228; PIDN:CAA41849.1; PID:g57229
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.2%; Score 14; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.8e-05; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 FRELHCTRYNIHMH 69
|||||
Db 167 FRELHCTRYNIHMH 180
|||||

RESULT 9
A39285
calcitonin receptor-la precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004
C;Accession: A39285; I47129
R;Lin, H.Y.; Harris, T.L.; Flannery, M.S.; Aruffo, A.; Kaji, E.H.; Gorn, A.; Kolakowski
Science 254, 1022-1024, 1991
A;Title: Expression cloning of an adenylate cyclase-coupled calcitonin receptor.
A;Reference number: A39285; MUID:92054591; PMID:1658940
A;Accession: A39285
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-482 <LIN>
A;Cross-references: UNIPROT:P25117; GB:M74420; NID:g164430; PIDN:AAA31023.1; PID:g164431
R;Zolnierowicz, S.; Cron, P.; Solinas-Toldo, S.; Fries, R.; Lin, H.Y.; Hemmings, B.A.

J. Biol. Chem. 269, 19530-19538, 1994
A;Title: Isolation, characterization, and chromosomal localization of the porcine calcitonin receptor-1b - pig
A;Reference number: A53972; MUID:94308241; PMID:8034723
A;Accession: 147129
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-482 <ZOL>
A;Cross-references: EMBL:Z31356; NID:g531126; PIDN:CAA83232.1; PID:g531127
C;Genetics:
A;Introns: 17/3; 70/1; 107/1; 144/3; 175/2; 217/3; 269/1; 289/2; 311/3; 384/3; 398/3
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.2%; Score 14; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 FQGFVAILIYCFN 307
DB 383 FQGFVAILIYCFN 396
|||||

RESULT 10
I47130
calcitonin receptor-1b - pig
A;Title: Isolation, characterization, and chromosomal localization of the porcine calcitonin receptor-1b - pig
A;Reference number: A53972; MUID:94308241; PMID:8034723
A;Accession: 147130
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-498 <ZOL>
A;Cross-references: UNIPROT:P25117; EMBL:Z31356; NID:g531126; PIDN:CAA83233.1; PID:g531127
C;Genetics:
A;Introns: 17/3; 70/1; 107/1; 144/3; 175/2; 233/3; 285/1; 305/2; 327/3; 400/3; 414/3
C;Superfamily: glucagon receptor

Query Match 3.2%; Score 14; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 FQGFVAILIYCFN 307
DB 399 FQGFVAILIYCFN 412
|||||

RESULT 11
I53273
gastric inhibitory polypeptide receptor - rat
A;Title: Isolation, characterization, and chromosomal localization of the porcine calcitonin receptor-1b - pig
A;Reference number: A53972; MUID:94308241; PMID:8034723
A;Accession: 153273
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-455 <RES>
A;Cross-references: UNIPROT:P43219; GB:L19660; NID:g431448; PIDN:AAC37637.1; PID:g431449
C;Superfamily: glucagon receptor

Query Match 3.0%; Score 13; DB 2; Length 455;
Best Local Similarity 100.8%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 FRRLHCTRNVIH 68
|||||

Db 159 FRRLHCTRNVIH 171
|||||

RESULT 12
JC2462
gastric inhibitory polypeptide receptor - hamster
A;Alternate names: GIP receptor
C;Species: Cricetineae gen. sp. (hamster)
C;Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
A;Accession: JC2462
R;Yasuda, K.; Inagaki, N.; Yamada, Y.; Kubota, A.; Seino, S.; Seino, Y.
Biochem. Biophys. Res. Commun. 205, 1556-1562, 1994
A;Title: Hamster gastric inhibitory polypeptide receptor expressed in pancreatic islets
A;Reference number: JC2462; MUID:95110292; PMID:7811236
A;Accession: JC2462
A;Molecule type: mRNA
A;Residues: 1-462 <YAS>
A;Cross-references: DDBJ:D38103; NID:g644880; PIDN:BAA07284.1; PID:g765087
C;Superfamily: glucagon receptor
C;Keywords: receptor; transmembrane protein
F;136-157/Domain: transmembrane #status predicted <TM1>
F;167-186/Domain: transmembrane #status predicted <TM2>
F;215-238/Domain: transmembrane #status predicted <TM3>
F;252-274/Domain: transmembrane #status predicted <TM4>
F;292-315/Domain: transmembrane #status predicted <TM5>
F;339-357/Domain: transmembrane #status predicted <TM6>
F;383-394/Domain: transmembrane #status predicted <TM7>

Query Match 3.0%; Score 13; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 FRRLHCTRNVIH 68
DB 159 FRRLHCTRNVIH 171
|||||

RESULT 13
G02234
gastric inhibitory polypeptide receptor - human
A;Alternate names: GIP receptor
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
A;Accession: G02234
R;Bonner, T.I.; Usdin, T.B.
submitted to the EMBL Data Library, October 1995
A;Reference number: G09336
A;Accession: G02234
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-466 <BON>
A;Cross-references: UNIPROT:P48546; EMBL:U39231; NID:g1066050; PIDN:AAA84418.1; PID:g1066050
C;Genetics:
A;Gene: GDB:GIPR
A;Cross-references: GDB:335023
A;Map position: 19q13.3-19q13.3
C;Superfamily: glucagon receptor

Query Match 2.8%; Score 12; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 FRRLHCTRNVIH 67
DB 162 FRRLHCTRNVIH 173
|||||

RESULT 14
S66676
glucose-dependent insulinotropic protein receptor precursor - human
A;Title: Isolation, characterization, and chromosomal localization of the porcine calcitonin receptor-1b - pig
A;Reference number: A53972; MUID:94308241; PMID:8034723
A;Accession: 147129
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-482 <ZOL>
A;Cross-references: EMBL:Z31356; NID:g531126; PIDN:CAA83232.1; PID:g531127
C;Genetics:
A;Introns: 17/3; 70/1; 107/1; 144/3; 175/2; 217/3; 269/1; 289/2; 311/3; 384/3; 398/3
C;Superfamily: glucagon receptor
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.2%; Score 14; DB 2; Length 482;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 FQGFVAILIYCFN 307
DB 383 FQGFVAILIYCFN 396
|||||

RESULT 10
I47130
calcitonin receptor-1b - pig
A;Title: Isolation, characterization, and chromosomal localization of the porcine calcitonin receptor-1b - pig
A;Reference number: A53972; MUID:94308241; PMID:8034723
A;Accession: 147130
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-498 <ZOL>
A;Cross-references: UNIPROT:P25117; EMBL:Z31356; NID:g531126; PIDN:CAA83233.1; PID:g531127
C;Genetics:
A;Introns: 17/3; 70/1; 107/1; 144/3; 175/2; 233/3; 285/1; 305/2; 327/3; 400/3; 414/3
C;Superfamily: glucagon receptor

Query Match 3.2%; Score 14; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 294 FQGFVAILIYCFN 307
DB 399 FQGFVAILIYCFN 412
|||||

RESULT 11
I53273
gastric inhibitory polypeptide receptor - rat
A;Title: Isolation, characterization, and chromosomal localization of the porcine calcitonin receptor-1b - pig
A;Reference number: A53972; MUID:94308241; PMID:8034723
A;Accession: 153273
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-455 <RES>
A;Cross-references: UNIPROT:P43219; GB:L19660; NID:g431448; PIDN:AAC37637.1; PID:g431449
C;Superfamily: glucagon receptor

Query Match 3.0%; Score 13; DB 2; Length 455;
Best Local Similarity 100.8%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 FRRLHCTRNVIH 68
|||||

R;Volz, A.; Goeke, R.; Lankat-Buttgereit, B.; Fehmann, H.C.; Bode, H.P.; Goeke, B.
FEBS Lett. 373, 23-29, 1995
A;Title: Molecular cloning, functional expression, and signal transduction of the GIP-re
A;Reference number: S66676; MUID:96013879; PMID:7589426
A;Accession: S66676
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-466 <VOL>
A;Cross-references: UNIPROT:P48546; GB:S79852
A;Note: the authors translated the codon GCC for residue 427 as Leu
C;Superfamily: glucagon receptor
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-466/Product: glucose-dependent insulinotropic protein receptor #status predicted <M

Query Match 2.8%; Score 12; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 FRLHCTRNYYH 67
| | | | | | | | | |
Db 162 FRLHCTRNYYH 173

RESULT 15

I37411
glucose-dependent insulinotropic polypeptide receptor - human
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 24-Sep-1999
C;Accession: I37411
R;Gremlich, S.; Porret, A.; Hani, E.H.; Cherif, D.; Vionnet, N.; Froguel, P.; Thorens, B.
Diabetes 44, 1202-1208, 1995
A;Title: Cloning, functional expression, and chromosomal localization of the human pancr
A;Reference number: I37411; MUID:96007224; PMID:7556958
A;Accession: I37411
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-491 <RES>
A;Cross-references: EMBL:X81832; NID:g1030050; PIDN:CAA57426.1; PID:g1030051
C;Superfamily: glucagon receptor

Query Match 2.8%; Score 12; DB 2; Length 491;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 FRLHCTRNYYH 67
| | | | | | | | | |
Db 161 FRLHCTRNYYH 172

Search completed: July 4, 2005, 06:29:04
Job time : 28 secs

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OM protein - protein search, using sw model

Run on: July 4, 2005, 06:17:00 ; Search time 91 Seconds
(without alignments)
2447.851 Million cell updates/sec

Title: US-09-869-565-2
Perfect score: 435
Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGARPPPLLOQGWETVM 435

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 1612378 seqs, 512079187 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	404	92.9	591	1 PTHR RAT	P25961 rattus norv
2	341	78.4	591	2 Q80WU8	Q80WU8 mus musculu
3	338	77.7	591	2 Q91WV4	Q91WV4 mus musculu
4	318	73.1	591	1 PTHR MOUSE	P41593 mus musculu
5	141	32.4	147	2 Q76N28	Q76N28 rattus norv
6	49	11.3	593	1 PTHR HUMAN	Q03431 homo sapien
7	49	11.3	595	2 Q9TU31	Q9TU31 canis fami
8	46	10.6	585	1 PTHR PIG	P50133 sus scrofa
9	43	9.9	589	2 Q9GMD1	Q9GMD1 oryctolagus
10	43	9.9	964	2 Q8NHB4	Q8NHB4 homo sapien
11	40	9.2	589	2 Q7YR13	Q7YR13 cervus elap
12	34	7.8	585	1 PTHR DIDMA	P25107 didelphis m
13	28	6.4	536	2 Q9PVD3	Q9PVD3 brachydanio
14	27	6.2	94	2 Q9PRG1	Q9PRG1 ictalurus p
15	26	6.0	126	2 Q57671	Q57671 meleagris g
16	25	5.7	575	2 Q9PBW7	Q9PBW7 brachydanio
17	18	4.1	542	2 Q9PVD2	Q9PVD2 brachydanio
18	18	4.1	546	1 PTHR MOUSE	Q91V95 mus musculu
19	18	4.1	546	1 PTHR RAT	P70555 rattus norv
20	18	4.1	550	1 PTHR HUMAN	P49190 homo sapien
21	15	3.4	24	2 Q71UK6	Q71UK6 homo sapien
22	14	3.2	440	1 SCRC HUMAN	Q47872 homo sapien
23	14	3.2	440	1 SCRC HUMAN	Q47872 homo sapien
24	14	3.2	445	1 SCRC RABIT	Q46502 oryctolagus
25	14	3.2	449	1 SCRC RAT	P23811 rattus norv
26	14	3.2	498	1 CALR PIG	P25117 sus scrofa
27	13	3.0	162	2 Q80UB4	Q80UB4 mus musculu
28	13	3.0	169	2 Q9R1D4	Q9R1D4 mus musculu
29	13	3.0	455	1 GIPR RAT	P43219 rattus norv
30	13	3.0	462	1 GIPR MESAU	P43218 mesocricetu
31	12	2.8	425	2 Q802T7	Q802T7 fugu rubrip

RESULT 1

ID	PTHR RAT	STANDARD	PRT	591 AA
AC	P25961			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Parathyroid hormone/parathyroid hormone-related peptide receptor			
DE	precursor (PTH/PTHr receptor) (PTH/PTHr type I receptor).			
GN	Name=Pthr1; Synonyms=Pthr,			
OS	Rattus norvegicus (Rat).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Bone;			
RX	MEDLINE=92212903; PubMed=1313566;			
RA	Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,			
RA	Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr.,			
RA	Kronenberg H.M., Segre G.V.;			
RT	"Expression cloning of a common receptor for parathyroid hormone and			
RT	parathyroid hormone-related peptide from rat osteoblast-like cells: a			
RT	single receptor stimulates intracellular accumulation of both cAMP and			
RL	inositol triphosphates and increases intracellular free calcium.";			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94292182; PubMed=8020952;			
RA	Pausova Z., Bourdon J., Clayton D., Mattei M.-G., Seldin M.F.,			
RA	Janicic N., Riviere M., Szpirer J., Levan G., Szpirer C.;			
RT	"Cloning of a parathyroid hormone/parathyroid hormone-related peptide			
RT	receptor (PTHr) cDNA from a rat osteosarcoma (UMR 106) cell line:			
RT	chromosomal assignment of the gene in the human, mouse, and rat			
RT	genomes.";			
RL	Genomics 20:20-26(1994).			
CC	-I- FUNCTION: This is a receptor for parathyroid hormone and for			
CC	parathyroid hormone-related peptide. The activity of this receptor			
CC	is mediated by G proteins which activate adenylyl cyclase and also			
CC	a phosphatidylinositol-calcium second messenger system.			
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-I- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; M77184; AAA1811.1; -;			
DR	EMBL; L19475; AAA68098.1; -;			
DR	PIR; I54195; I54195.			

Q64FL4 oncorhynchu
P48546 homo sapien
Q91BG2 gallus gall
Q8AXV3 fugu rubrip
Q64FL3 oncorhynchu
Q9VHC6 rana ridibu
Q90308 carassius a
P32241 homo sapien
Q91085 meleagris g
Q6P2M6 homo sapien
Q28992 sus scrofa
P57751 mus musculu
P30093 rattus norv
Q9J1Y4 mus musculu

ALIGNMENTS


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Db 242 AVLYSGFTLDEARLLEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYLATNYWILV 301
QY 146 EGLYLSLIFMAFFSEKKYLWGFTIFGWLGPVAVFVAVVWVRATLANTGCDLSSGHKKW 205
Db 302 EGLYLSLIFMAFFSEKKYLWGFTIFGWLGPVAVFVAVVWVRATLANTGCDLSSGHKKW 361
QY 206 IIQVPILASVNLNFIILFINIRVLATKLRETNAGCDTROQYRKLRLSTLVLPFGVHY 265
Db 362 IIQVPILASVNLNFIILFINIRVLATKLRETNAGCDTROQYRKLRLSTLVLPFGVHY 421
QY 266 TVFMALPYTEVSGTLQIQWHYEMLFNSFGQFFVAILIYFCNCEVQAEIRKSRWTLAL 325
Db 422 TVFMALPYTEVSGTLQIQWHYEMLFNSFGQFFVAILIYFCNCEVQAEIRKSRWTLAL 481
QY 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSRL 366
Db 482 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSRL 522

RESULT 3
ID Q91WV4 PRELIMINARY; PRT; 591 AA.
AC Q91WV4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Parathyroid hormone receptor 1.
GN Name=Pthrl;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klugner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013446; AAH13446.1; -.
DR HSSP; Q03431; 1BL1.
DR MGD; MGI:17801; Pthrl.
DR GO; GO:0004991; P:parathyroid hormone receptor activity; TAS.
DR GO; GO:0030282; P:bone mineralization; IMP.
DR GO; GO:0001501; P:skeletal development; IMP.
DR Pfam; PF00002; 7tm2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR0249; GPCRSECRETIN.
DR PRINTS; PR00393; PTHORMONER.
DR SMART; SM0008; HORMR; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.

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DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor.
SQ SEQUENCE 591 AA; 66361 MW; 6E29CF63E5BAFED CRC64;

Query Match 77.7%; Score 338; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EVFDRLCMTYTVGYSMSLASLTAVLILAYFRLHCHTRNYIHHMFLSFMLRAASIFVKD 85
Db 182 EVFDRLCMTYTVGYSMSLASLTAVLILAYFRLHCHTRNYIHHMFLSFMLRAASIFVKD 241
QY 86 AVLYSGFTLDEARLLEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYLATNYWILV 145
Db 242 AVLYSGFTLDEARLLEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYLATNYWILV 301
QY 146 EGLYLSLIFMAFFSEKKYLWGFTIFGWLGPVAVFVAVVWVRATLANTGCDLSSGHKKW 205
Db 302 EGLYLSLIFMAFFSEKKYLWGFTIFGWLGPVAVFVAVVWVRATLANTGCDLSSGHKKW 361
QY 206 IIQVPILASVNLNFIILFINIRVLATKLRETNAGCDTROQYRKLRLSTLVLPFGVHY 265
Db 362 IIQVPILASVNLNFIILFINIRVLATKLRETNAGCDTROQYRKLRLSTLVLPFGVHY 421
QY 266 TVFMALPYTEVSGTLQIQWHYEMLFNSFGQFFVAILIYFCNCEVQAEIRKSRWTLAL 325
Db 422 TVFMALPYTEVSGTLQIQWHYEMLFNSFGQFFVAILIYFCNCEVQAEIRKSRWTLAL 481
QY 326 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLS 363
Db 482 DFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLS 519

RESULT 4
PTHR_MOUSE
ID PTHR_MOUSE STANDARD; PRT; 591 AA.
AC P41593; Q62119;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
GN Names=Pthrl; Synonyms=Pthr;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEHA;
RX MEDLINE=95034305; PubMed=7524627; DOI=10.1016/0925-4773(94)90093-0;
RA Karperien M., van Dijk T.B., Hosijsmakers T., Cremers F.,
RA Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;
RT "Expression pattern of parathyroid hormone/parathyroid hormone related
RT peptide receptor mRNA in mouse postimplantation embryos indicates
RT involvement in multiple developmental processes.";
RL Mech. Dev. 47:29-42(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=94255468; PubMed=8197183;
RA McCuaig K.A., Clarke J.C., White J.H.;
RT "Molecular cloning of the gene encoding the mouse parathyroid
RT hormone/parathyroid hormone-related peptide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:5051-5055(1994).
CC -1- FUNCTION: This is a receptor for parathyroid hormone and for
CC parathyroid hormone-related peptide. The activity of this receptor
CC is mediated by g proteins which activate adenylyl cyclase and also
CC a phosphatidylinositol-calcium second messenger system.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.

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ID	PTHR HUMAN	STANDARD;	PRT;	593 AA.
AC	Q03431;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Parathyroid hormone/parathyroid hormone-related peptide receptor			
DE	precursor (PTH/PTHrP receptor) (PTH/PTHrP type I receptor).			
GN	Name=PTHRI; Synonyms=PTHr;			
OS	Homo sapiens (Human)			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=93238641; PubMed=8386612; DOI=10.1210/en.132.5.2157;			
RA	Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,			
RA	Abou-Samra A.-B., Segre G.V., Jueppner H.;			
RT	"Identical complementary deoxyribonucleic acid encode a human renal			
RT	and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";			
RL	Endocrinology 132:2157-2165(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=93387403; PubMed=8397094; DOI=10.1016/0922-4106(93)90092-N;			
RA	Schneider H., Feyen J.-H., Rao Movva N.;			
RT	"Cloning and functional expression of a human parathyroid hormone			
RT	receptor.";			
RL	Eur. J. Pharmacol. 246:149-155(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95263723; PubMed=7745008; DOI=10.1210/jc.80.5.1611;			
RA	Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,			
RA	Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C.,			
RA	Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,			
RA	Abou-Samra A.-B., Segre G.V., Jueppner H.;			
RT	"Pseudohypoparathyroidism type Ib is not caused by mutations in the			
RT	coding exons of the human parathyroid hormone (PTH)/PTH-related			
RT	peptide receptor gene.";			
RL	J. Clin. Endocrinol. Metab. 80:1611-1621(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RA	Levine M.A.;			
RT	"Characterization of cDNA and genomic DNA encoding the human PTH/PTHrP			
RT	receptor.";			
RL	Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	EXTRACELLULAR DOMAIN DISULFIDE BONDS.			
RX	MEDLINE=20374568; PubMed=10913300; DOI=10.1021/bi0001426;			
RA	Grauschopf U., Lillie H., Honold K., Wozny M., Reusch D., Esswein A.,			
RA	Schafer W., Rucknagel K.P., Rudolph R.;			
RT	"The N-terminal fragment of human parathyroid hormone receptor 1			
RT	constitutes a hormone binding domain and reveals a distinct disulfide			
RT	pattern.";			
RL	Biochemistry 39:8878-8887(2000).			
RN	[6]			
RP	STRUCTURE BY NMR OF 169-198.			
RX	MEDLINE=98409426; PubMed=9737850; DOI=10.1021/bi981265h;			
RA	Pellegrini M., Bisello A., Rosenblatt M., Chorev M., Mierke D.F.;			
RT	"Binding domain of human parathyroid hormone receptor: from			
RT	conformation to function.";			
RL	Biochemistry 37:12737-12743(1998).			
RN	[7]			
RP	VARIANT JMC ARG-223.			
RX	MEDLINE=95215874; PubMed=7701349;			
RA	Schipani E., Kruse K., Jueppner H.;			
RT	"A constitutively active mutant PTH-PTHrP receptor in Jansen-type			
RT	metaphyseal chondrodysplasia.";			
RL	Science 268:98-100(1995).			
RN	[8]			
RP	VARIANTS JMC ARG-223 AND PRO-410.			
RX	MEDLINE=96366745; PubMed=8703170; DOI=10.1056/NEJM199609053351004;			

RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
RA Kooh S.W., Cole W.G., Jueppner H.;

RT "Constitutively activated receptors for parathyroid hormone and
RT parathyroid hormone-related peptide in Jansen's metaphyseal
RT chondrodysplasia.";

RL N. Engl. J. Med. 335:708-714(1996).

RN [9]

RP CHARACTERIZATION OF VARIANTS JMC ARG-223 AND PRO-410.

RX MEDLINE=97322091; PubMed=9178745; DOI=10.1210/me.11.7.851;

RA Schipani E., Jensen G.S., Pincus J., Nissen R.A., Gardella T.J.,
RA Jueppner H.;

RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate
RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide
RT receptors mutated at the two loci for Jansen's metaphyseal
RT chondrodysplasia.";

RL Mol. Endocrinol. 11:851-858(1997).

RN [10]

RP VARIANT BOCD LSU-132.

RX MEDLINE=98417978; PubMed=9745456; DOI=10.1210/jc.83.9.3373;

RA Zhang P., Jobert A.-S., Couvineau A., Silve C.;

RT "A homozygous inactivating mutation in the parathyroid
RT hormone/parathyroid hormone-related peptide receptor causing
RT Blomstrand chondrodysplasia.";

RL J. Clin. Endocrinol. Metab. 83:3365-3368(1998).

RN [11]

RP VARIANT JMC ARG-458.

RX MEDLINE=99415605; PubMed=10487664; DOI=10.1210/jc.84.9.3052;

RA Schipani E., Langman C.B., Hunzelman J., Le Merrer M., Loke K.Y.,
RA Dillon M.J., Silve C., Jueppner H.;

RT "A novel parathyroid hormone (PTH)/PTH-related peptide receptor
RT mutation in Jansen's metaphyseal chondrodysplasia.";

RL J. Clin. Endocrinol. Metab. 84:3052-3057(1999).

RN [12]

RP VARIANT ENCHONDROMATOSIS CVS-150.

RX MEDLINE=21918585; PubMed=11850620; DOI=10.1038/ng844;

RA Hopyan S., Gokgoz N., Poon R., Gensure R.C., Yu C., Cole W.G.,
RA Bell R.S., Jueppner H., Andrulis I.L., Wunder J.S., Alman B.A.;

RT "A mutant PTH/PTHrP type I receptor in enchondromatosis.";

RL Nat. Genet. 30:306-310(2002).

CC -I- FUNCTION: This is a receptor for parathyroid hormone and for
CC parathyroid hormone-related peptide. The activity of this receptor
CC is mediated by G proteins which activate adenylyl cyclase and also
CC a phosphatidylinositol-calcium second messenger system.

CC -I- SUBCELLULAR LOCATION: Integral membrane protein.

CC -I- TISSUE SPECIFICITY: Expressed in most tissues. Most abundant in
CC kidney, bone and liver.

CC -I- DISEASE: Defects in PTHRI are the cause of Jansen's metaphyseal
CC chondrodysplasia (JMC) [MIM:156400]. JMC is a rare autosomal
CC dominant disorder characterized by a short-limbed dwarfism
CC associated with hypercalcemia and normal or low serum
CC concentrations of the two parathyroid hormones.

CC -I- DISEASE: Defects in PTHRI are the cause of chondrodysplasia
CC Blomstrand type (BOCD) [MIM:215045]. BOCD is a severe skeletal
CC dysplasia.

CC -I- DISEASE: Defects in PTHRI can be a cause of enchondromatosis
CC [MIM:166000]. Enchondromas are common benign cartilage tumors of
CC bone. They can occur as solitary lesions or as multiple lesions in
CC enchondromatosis (Ollier and Maffucci diseases). Clinical problems
CC caused by enchondromas include skeletal deformity and the
CC potential for malignant change to osteosarcoma.

CC -I- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; L04308; AAA36525.1; -;
DR EMBL; X68596; CAA48589.1; -;
DR EMBL; U22409; AAB60657.1; -;


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DR EMBL; U22401; AAB60657.1; JOINED.
DR EMBL; U22402; AAB60657.1; JOINED.
DR EMBL; U22403; AAB60657.1; JOINED.
DR EMBL; U22404; AAB60657.1; JOINED.
DR EMBL; U22405; AAB60657.1; JOINED.
DR EMBL; U22406; AAB60657.1; JOINED.
DR EMBL; U22407; AAB60657.1; JOINED.
DR EMBL; U22408; AAB60657.1; JOINED.
DR EMBL; U17418; AAB56774.1; -.
DR PIR; I38139; A49191.
DR PDB; 1BLJ; NMR; @=168-198.
DR PDB; 1ET2; Model; S=168-469.
DR PDB; 1ET3; Model; S=168-469.
DR Genew; HGNC:9608; PTHR1.
DR MIM; 168468; -.
DR MIM; 156400; -.
DR MIM; 215045; -.
DR MIM; 166000; -.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0004991; P:parathyroid hormone receptor activity; TAS.
DR GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.
DR GO; GO:0001501; P:skeletal development; TAS.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
DR 3D-structure; Disease mutation; Dwarfism; G-protein coupled receptor;
KW Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 26
FT CHAIN 27 593
FT DOMAIN 27 188 Parathyroid hormone/parathyroid hormone-
FT TRANSMEM 189 212 related peptide receptor.
FT DOMAIN 213 219 Extracellular (Potential).
FT TRANSMEM 220 239 1 (Potential).
FT DOMAIN 240 282 2 (Potential).
FT TRANSMEM 283 306 Extracellular (Potential).
FT DOMAIN 307 320 3 (Potential).
FT TRANSMEM 321 342 Cytoplasmic (Potential).
FT DOMAIN 343 361 Extracellular (Potential).
FT TRANSMEM 362 382 4 (Potential).
FT DOMAIN 383 409 5 (Potential).
FT TRANSMEM 410 428 Cytoplasmic (Potential).
FT DOMAIN 429 440 6 (Potential).
FT TRANSMEM 441 463 Extracellular (Potential).
FT DOMAIN 464 593 7 (Potential).
FT TRANSMEM 464 593 Cytoplasmic (Potential).

Query Match 11.3%; Score 49; DB 1; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFYFLATNYWILVEGLYHLSIFMAFFSEKKYLGFT 169
Db 277 GYACRVAVTFYFLATNYWILVEGLYHLSIFMAFFSEKKYLGFT 325

RESULT 7
Q9TU31 PRELIMINARY; PRT; 595 AA.
AC Q9TU31
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Parathyroid hormone receptor-1.
GN Name=PTH1;

Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167095; AAD55938.1; -.
DR HSSP; Q03431; 1BL1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004991; F:parathyroid hormone receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR002170; Phrmn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR SMART; SM00008; Hormr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS02227; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECEP_F2_4; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 595 AA; 66308 MW; 09568ECF38D4D258 CRC64;

Query Match 11.3%; Score 49; DB 2; Length 595;
Best Local Similarity 100.0%; Pred. No. 1.8e-38;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 121 GYACRVAVTFYFLATNYWILVEGLYHLSIFMAFFSEKKYLGFT 169
Db 276 GYACRVAVTFYFLATNYWILVEGLYHLSIFMAFFSEKKYLGFT 324

RESULT 8
PTTR_PIG STANDARD; PRT; 585 AA.
ID PTTR_PIG
AC P50133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE Precursor (PTH/PTHr receptor) (PTH/PTHr type I receptor).
GN Name=PTHr1; Synonyms=PTHr;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96305358; PubMed=8688470; DOI=10.1016/0167-4781(96)00035-8;
RA Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,
RA Chandrasekhar S., Hsiung H.M.;
RT "Structure and functional expression of a complementary DNA for
RT porcine parathyroid hormone/parathyroid hormone-related peptide
RT receptor.";
RL Biochim. Biophys. Acta 1307:339-347(1996).
CC -!- FUNCTION: This is a receptor for parathyroid hormone and for
CC parathyroid hormone-related peptide. The activity of this receptor
CC is mediated by G proteins which activate adenylyl cyclase and also
CC a phosphatidylinositol-calcium second messenger system (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
CC
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[illegible]

"Zebrafish express the common parathyroid hormone/parathyroid hormone-related peptide receptor (PTH1R) and a novel receptor (PTH3R) that is preferentially activated by mammalian and fugu fish parathyroid hormone-related peptide.";
J. Biol. Chem. 274:28185-28190 (1999).

DR EMBL; AF132084; AAF01265.1; -;
DR HSSP; Q03431; 1BL1.
DR ZFIN; ZDB-GENE-991123-8; pthrl.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004930; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004991; F:parathyroid hormone receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; Hormn_receptor.
DR InterPro; IPR002170; Phrmn_receptor.
DR Pfam; PF00002; 7tm 2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00393; PTHORMONER.
DR SMART; SM00008; HormR; 1.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECP_F2_3; 1.
DR PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.
KW Receptor.

SQ SEQUENCE 536 AA; 61454 MW; 653B0A56DB2C8FA9 CRC64;

Query Match 6.4%; Score 28; DB 2; Length 536;

Best Local Similarity 100.0%; Pred. No. 4.9e-18; Mismatches 0; Indels 0; Gaps 0;

Matches 28; Conservative 0;

Qy 224 NIIRVATKLRETNAGRCDDTQVYRKL 251

Db 334 NIIRVATKLRETNAGRCDDTQVYRKL 361

RESULT 14

O9PRG1

ID O9PRG1 PRELIMINARY; PRT; 94 AA.

AC O9PRG1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Parathyroid hormone type-2 receptor (Fragment).

OS Ictalurus punctatus (Channel catfish).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;

OC Ictaluridae; Ictalurus.

OX NCBI_TaxID=7998;

RP [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RC MEDLINE=99367425; PubMed=10438471; DOI=10.1074/jbc.274.33.23035;

RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;

RT "A G protein-coupled receptor from zebrafish is activated by human

parathyroid hormone and not by human or teleost parathyroid hormone-

related peptide. Implications for the evolutionary conservation of

calcium-regulating peptide hormones";

J. Biol. Chem. 274:23035-23042 (1999).

DR EMBL; AF132081; AAD51907.1; -;

DR EMBL; AF132078; AAD51906.1; -;

DR EMBL; AF132079; AAD51906.1; JOINED.

DR EMBL; AF132080; AAD51906.1; JOINED.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004930; F:G-protein coupled receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR000832; GPCR_secretin.

Pfam; PF00002; 7tm 2; 1.

PRINTS; PR00249; GPCRSECRETIN.

PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.

Receptor.

KW Receptor.

FT NON_TER 1 94

FT NON_TER 94 94

SQ SEQUENCE 94 AA; 10729 MW; D949182E1D2613EF CRC64;

Query Match 6.2%; Score 27; DB 2; Length 94;

Best Local Similarity 100.0%; Pred. No. 1e-17;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 YPLATNYWILVEGLYLSLIFMAFPPS 160

Db 12 YPLATNYWILVEGLYLSLIFMAFPPS 38

RESULT 15

O57671

ID O57671 PRELIMINARY; PRT; 126 AA.

AC O57671;

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Parathyroid hormone receptor (Fragment).

OS Meleagris gallopavo (Common turkey).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.

OX NCBI_TaxID=9103;

RP [1]

RP SEQUENCE FROM N.A.

RA Hsu C., You S., El Halawani M.E., Foster D.N.;

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U94326; AAB93893.1; -;

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004930; F:G-protein coupled receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR000832; GPCR_secretin.

Pfam; PF00002; 7tm 2; 1.

PRINTS; PR00249; GPCRSECRETIN.

PROSITE; PS0261; G_PROTEIN_RECP_F2_4; 1.

Receptor.

KW Receptor.

FT NON_TER 1 126

FT NON_TER 126 126

SQ SEQUENCE 126 AA; 14515 MW; 0F381BDB094A1A77 CRC64;

Query Match 6.0%; Score 26; DB 2; Length 126;

Best Local Similarity 100.0%; Pred. No. 1.2e-16;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 144 LVEGLYLSLIFMAFFSEKKYLGFT 169

Db 6 LVEGLYLSLIFMAFFSEKKYLGFT 31

Search completed: July 4, 2005, 06:30:44

Job time : 96 secs

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